

Release 2.1D John F. Collins, Biocomputing Research Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Peb 24 07-16-02 1949; MasPar time 9 08 Seconds 422.695 Million cell updates/sec Pur on.

Tabular output not generated.

>US-08-844-215-7 (1-125) from US09844215 pep 949

Description: Perfect Score:

1 EVQLLESGSEVKKPGSSVKV Sequence.

GSCWGWFDPWGQGTLVTVSS 126

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Mean 40.893; Variance 107.589; scale 0.380 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ID Description Pred. No.	heavy chain V reg 4.	q heavy chain V red 4.62e-8	q heavy chain V-1 r 1.66e-8	chain V req	Theavy thain V red 1,75e-7	q heavy chain V req 3,57e-7	q heavy chain V-1 r 1.49e-7	q heavy chain V req 1.49e-7	g heavy chain V reg 4 37e-7	Iq heavy chain V req 6.24e-7	Ig heavy chain V reg 2.	Ig heavy chain V reg 3.72e-7	Iq heavy chain V-1 r 5.32e-7	Iq mu chain precurso 5.32e-7	Ig heavy chain V reg 1.55e-7	q heavy chain precu 1.	Ig heavy chain V-D-J 1.55e-7	61 Ig heavy chain V reg 2.22e-7	Iq heavy chain V1 re 3.17e-7	
DB	5 7	7	29 7	16 7	r-	20 7	26 7	27 7	7 25	7	21 7	35 7	33 7	7 7	7	16 7	3 7	16 7 836	8 7 \$24	
% Query Match Length			69.7	69.2	683	68.1	٠.	67.7	€ 29							66.3				
Score	754	671	661	657	648	646	642	642	639	638	634	633	632	632	629	629	629	879	627	
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3.86e-75	.51e-7	.61e-7	.85e-7	.28e-7	.18e-7	.18e-7	.97e-7	.42e-6	130-6	.20e-6	.01e-6	.94e-6	.94e-6	.01e-6	.05e-6	.93e-6	.17e-6	.94e-6	01e-6	.43e-5	.19e-6	.19e-6	.70e-6	450-6
cavy chai	g heavy chain V-D	g heavy chain V r	g heavy chain V1	g heavy chain pro	g heavy chain V-I	g heavy chain V r	g heavy chain V r	g heavy chain V r	nti-PRZ erythrocy	g heavy chain V r	q heavy chain V-I	g heavy chain V r	q heavy chain V-1	g heavy chain V r	g heavy chain V r	g heavy chain V r	q heavy chain V r	g heavy chain V r	g heavy chain V r	q heavy chain V r	g heavy chain V r	g heavy chain V z	q heavy chain V r	g heary chain V r
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5.3	.2	.9	.7 3	.4 13	.3 11	.3 12	.6 12	.5	.2 16	.9 11	e.	.7 10	.7 12	.9 12	.7 12	.6 12	.5 10	.4 17	1 5	.4 12	.8 12	.8 14	.7 12	11 3.
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ALIGNMENTS

DATE 17-1993 #sequence_revision 17-Apr-1993 #text_change ACCESSIONS PH0957 PH0957 #32.LD. #33.LD. #34.LD. #34.	1 4741745Garvekpgssykysokagggdissyalderigapggggggggggggggggggggggggggggggggggg
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1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	61 aqkfqgrvtitadestntaymelsslrsedtavyycard-gcsgqscyfwgwfdpwgq

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*superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc Natl Acad Sci U.S.A. (1989, A6.5913-5917
Developmentually restricted immunoglobulin heavy chain
variable region gene expressed at high frequency in chroniv-
lymphocytic leukemia.
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                   PH0952 *type fragment | Ig heavy chain V region (64 CLL-SMI) - human (fragment) | Heavy chain V region (64 CLL-SMI) - human (fragment) | Hformal name Homo sapiens #common_name man | 17.Apr-1991 *sequence_revision 17.Apr-1993 *text_change
                                                                                                                                                                             *authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#tille Evidence for somatic selection of natural autoantibodies
#cross-references MUID:92202880
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J. Exp. Med. (1992) 175:983-991
Evidence for somatic selection of natural autoantibodies.
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Ig heavy chain V-1 region (NEI) - human
#formal_name Homo sapiens #common_name man
17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
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                                                                                                                                                                                                                                                                                                                     #authors Martin, I.: Duffy, S.F.: Carson, D.A.: Kipps, I.J.
#journal J. Exp. Med. (1992) 175:983-991
#tille Evidence for Sometic Selection of natural autoantibodies.
#cross-references MuID:92202880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (G6+ T-L26) - human (fragment) #formal_name Homo sapiens #common_name man 17.Apr-1993 #sequence_revision 17.Apr-1993 #text_change 15.Aug-1996
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#length 129 #molecular-weight 13932 #checksum 3075
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Pred. No. 1.66e-81;
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                                                                                                                                                                                     #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
Exp. Med. (1992) 175:983-991
Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MID:92202880
#accession PH0958
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#journal J. Exp. Med. (1992) 175:983:991
#ittle Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
                                                   PH0958 *type fragment Ig heavy chain V region (G6+ CLL-HUR) - human (fragment) *fformal_name Homo sapiens #common_name man 17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change
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Pred. No. 1.75e-79;
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Best Local Similarity 77.0%;
Matches 97; Conservative
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##experimental_source the sequence was determined from the differentiated gene FICATION #superfamily immunoglobulin V region; immunoglobulin homology bbs heterotetramer; immunoglobulin
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Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
#formal_name Homo sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
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#title Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in 1ymphocytic leukemia.
#cross-references MUID:89345575
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Ig heavy chain V-1 region (AND) - human
                                                  Query Match 68.1%; Score 546; DB 7; 1
Best Local Similarity 77.8%; Pred. No. 3.57e-79;
Matches 98; Conservative 13; Mismatches 9.
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Best Local Similarity 74.6%; Pred. No. 1.49e-78;
Matches 94; Conservative 12; Mismatches 20,
#length 120 #checksum 5559
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#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies
#cross.references MUID:92202880
#across.references MUID:92202880
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J. Exp. Med. (1992) 175:983-991
Evidence for somatic selection of natural autoantibodies
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Pred. No. 4.37e-78;
16; Mismatches 14; Indels
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#region complementarity-determining 3
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*Superfamily immanuglobulin V region; immunoglobulin homology
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06-oct-1994 #sequence_revision 18-Nov-1994 #text_change
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Burton, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #title Recombinant human Fab to glycoprotein D neutralizes infectivity and prevents cell-to-cell transmission of herpes simplex viruses 1 and 2 in vitro. #accession A49590 #statue
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Ig heavy chain V region (G6+ T-L33) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. 
J. Exp. Med. (1992) 175:983-991
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                                                                                                                                                                                                                          61 ggrvtftadaststaymelsslrsedtavyycarv-g-ycstngcslggmdvwgggttvi 118
                                                                                                                                                                                                                                            65 QGRVIITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSCW-GWFDPWGQGTLVT 123
                                                                                                                                                                                                                                                                                                                                                                                                PH0953 #type fragment
Ig heavy chain V region (%6+ CLL-SIC) - human (fragment)
#formal_name Homo sapiens #common_name man
17-Apr-1993 *sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J Exp Med. (1992) 175-982-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
                                                                                                                                                 1 lesgaevkkpgssvkvscktsggafssyainwvrqapggglewmggilpvfgttnhaqkf 60
                                                                                                                                                                                     5 LESGSEVKKPGSSVKVSCRASGGSFRSYNFNWVRQAPGQGLEWMGGIIPMFGTANYAQKF 64
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                                                                                                                3; Gaps
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19 heavy chain V-1 region (783) - human
*formal_name Homo sapiens *common_name man
17-Jan-1990 *sequence_revision 17-Jan-1990 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 aqkfqgrvtitadeststaymelsslrsedtavyycarn-g-ycg-gdrysrw 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carson, D A
Proc. Natl. Acad. Sci. U.S A (1989) 85.5913-5917
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               #domain immunoglobulin homology #label 1MM
#length 121 #checksum 6226
                                                                  Score 634; DB 7; Length 121;
Pred No. 2.610-77;
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                                                                                                          12; Mismatches 16; Indels
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#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
#length 135 #checksum 2318
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                                                                        Query Match 66.8%;
Best Local Similarity 74 9%;
Matches 92; Conservative
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FEATURE
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FEATURE
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##experimental_source the sequence was determined from the differentiated gene tricATION #superfamily immunoglobulin V region; immunoglobulin homology NOS heteroteramer; immunoglobulin
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CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig mu chain precursor, membrane-bound (clone 201) - human #formal_name Homo sapiens #common_name man 31-Der-1091 #sequence_revision 31-Der-1091 #text_change
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Nucleic Acids Res (1990) 18-4278
Complete nucleotide sequence of the membrane form of the
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                                                                                                                                                        preliminary; nucleic acid sequence not shown; not
                                                                                                                                                                                                                                                                                                                                                                                                                               #domain immunoglobulin homology #label IMM
#length 133 #molecular-weight 14320 #checksum 1289
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Pred. No. 5.32e-77;
15; Mismatches 14; Indels
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                                                                                                                                                                                 compared with conceptual translation
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#cross-references MUID:90332450
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##residues 1-627 ##label FRI
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Best Local Similarity 72.9%;
Matches 97; Conservative
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114 DPWGQGTLVTVSS 126

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Winter, G.
J. Mol. Biol. (1992) 227:776-798
The repertoire of human germline V(H) sequences reveals about fifty groups of V(H) segments with different hypervariable solus.
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CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FBATURE
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                                   #type fragment

Ig heavy chain V region (DP-10) - human (fragment)

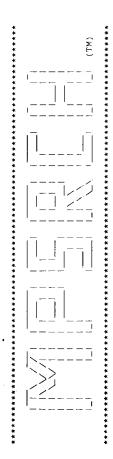
#formal_mame Homo sapiens #common_name man

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#title
RESULT 15
ENTRY
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Feb 24 07:42:43 1999; MasPar time 3.28 Seconds 195.669 Million cell updates/sec Pun on.

Tabular output not generated.

Description: Perfect Score:

>US-08-844-215-7 (1-126) from US08844215.pep 949 1 EVQLLESGSEVKKPGSSVKV Sequence:

GSCWGWFDPWGQGTLVTVSS 126

PAM 150 Gap 11 Scoring table:

56402 seqs, 5095871 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued l:backl 2.51 3.52 4.53 5.54 6.55 7.56 8:PCT90 9 PCT91 l0:PCT92 11.PCT93 12.PCT94 13:PCT95 14.PCT96

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 28.440; Variance 143 456; scale 0 198 Statistics:

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	635		120	11	PCT-US93-1	Sequence 13, Applicati	1.04e-42
8	609			11	PCT-US93-1	, Applica	**
٣	605	63.8	129	13	PCT-US95-0	45,	4
4	604		147	9	US-08-217-	4	p - 0
S	595	62.7		10	PCT-US92-0		140-3
9	595	Α.	102	۲-	US-08-053-	63	2.14e-39
7	595			C	FOT HISBD-1	۳.	2.140-33
α	595	62.7		۲	US-07-834-	55, Appli	33
6	591	ď.	117	7	US-08-474-	15,	.58e-3
10	591	62.3	117	ç	US-08-477-	10	4.58e-3
11	591	62.3	117	9	US-08-477-	4	4
12	591	ď	117	9	US-08-477-	15	4
13	591	62.3	117	(c)	US-08-477-	Sequence 72, Applicati	4.58
14	591	7	117	v	- 4 £ 9 - £ 3 4 -	ι. Γ.	4
15	591	•	117	9	US-07-634-	4, A	4.580-39
16	591	ά.	117	9	US-07-634-	72,	6-3
17	591	62.3	117	9	US-07-634-	104,	4.58e-39
18	591	ς.	117	/	US-08-474-	4, Ap	4.58e-39
19	591	٠	117	7	US-08-487-	15,	e-3
20	591	62.3	117	7	US-08-487-	72,	4.580-39
21	591	2	117	٢	US-08-474-	104	4 580-39
22	591	62.3	117	^	US-08-474-	72, Appli	9-3

4, Applicatio 4.58e-39 2, Applicatio 9.58e-39 63, Applicatio 9.31e-36 63, Applicati 6.31e-36 12, Applicati 1.48e-35 14, Applicatio 1.59e-34 16, Applicatio 1.59e-34 6, Applicatio 1.59e-34 6, Applicatio 1.59e-34 6, Applicatio 1.1e-34 6, Applicatio 4.11e-34 6, Applicatio 4.11e-34 10, Applicati 1.06e-33 11, Applicati 1.06e-33 11, Applicati 1.87e-33 13, Applicati 1.87e-33 13, Applicati 1.87e-33 13, Applicati 1.87e-33 13, Applicati 1.87e-33		NG PPODUCTION OF FAMILY PESTPICTED ANTIBODIES -CELL SUPERANTIGEN AND CONJUG 500 #1.25	
117 7 118-08-487 - Sequence 112 PCT 118-08-487 - Sequence 128 1 PCT 1285-1 Sequence 128 1 PCT 1285-1 Sequence 119 13 PCT 1385-0 Sequence 119 13 PCT 1385-0 Sequence 119 13 PCT 1385-0 Sequence 119 1 PCT 1385-1 Sequence 116 0 Sequence 111	ALIGNMENTS	9310555. 9310555. FOR STIMULATI E PRGION GENE TION WITH A B TION WITH A B East - Suite East - Suite 85-DCS 6 #1.0, VGzSi 893/10555	aming actus
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RESULT
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  APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIRODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
                                                                                                                                            9
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                                                                                                                                                                  1 VHLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVP, APPARTEWSTIPTFFF, ANYA 60
                                                                                                                                                                                       2 VQLLESGSEVKKPGSSVKVSCPASGSPPSYNFNWVPQAPGQGLEWMGGIPMHGIANYA 61
                                                                                                                                          7; Gaps
                                                                                                                   Length 120
                                                                                                                 Score 635; DB 11; Length 120
Pred. No. 1.04e-42;
15; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: PatentIn Pelease #1.0. Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Spensley Horn Jubas & Lubitz.
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                     PRT;
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29-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                               Application PC/TUS9310555
                                                                   NAME/KEY: Peptide
LOCATION: 1..120
NCE 120 AA; 13008 MW; 78865 CN;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application PC/THS0210555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STEAY L.
REGISTRATION NUMBER: 4.442
REFERENCE/DOCKET NUMBER: FD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 455-5100
TELEPTAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 51 CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 120 amino acids
amino acid
       TOPOLOGY linear
MOLECULE TYPE peptide
IMMEDIATE SOURCE
 STRANDEDNESS: single
                                                                                                           Ouery Match
Best Local Similarity 73.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                 PCT-US93-10555-12
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                                                                                                                                                                                                                                                             115 LVTVSS 120
                                                                                                                                                                                                                                                                                    121 LVTVSS 126
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                                              CLONE
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                                                          FEATURE:
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                                                                                             SEQUENCE
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61 QKFQGBVIITTDESISIAVMEVSSLRSEDTALYYGAPE-GRRMAINP----FDYWGQGTL. 115
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                                                                                                                                                                                                                                        5; Gaps
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TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                             Score 609; PR 11; Length 120;
Pred. No. 1.48e-40;

    Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 2000

                                                                                                                                                                                                                                        19; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARP: Patentin Poloase #1.5, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: PCT/US95/01219
25-JAN-1995
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45. Appliestice Profinescol219.
                                                                                                                                          ION: 1..120
120 AA; 12984 MW; 80846 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, William L. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 25-JAN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/LOCKET NUMBER -
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                                                                                                                                                                                               Query Match
Best Local Similarity 72.0%;
Matches 90; Conservative
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MEDIUM TYPE: Floppy
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California
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FILING DATE: 25-JAN
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                                                                                                                     NAME/KEY: Peptide
LOCATION: 1..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
          MOLECULE TYPE: Dent
                                                   IMMEDIATE SOURCE:
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STRANDEDNESS:
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                                                                            CLONE
                                                                                                 FEATURE:
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2; Gaps

84; Conservative 21; Mismatches 21; Indels

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                                                                                                                                                                                                                                                                                                                  60 YAQKFQGRVIITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSC-WG--WFDPW 116
                                                                                                                                                                                                                                                                                            61 YAQKFQGRVTITADISTSTAYMELSSLPSEDTAVYYCAPA-PGYGSGGGGYPGDYXFDYW 119
                                                                                                                                                                          5; Gaps
                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDIN 60
                                                                                                                                                                                                                                                   1 EVQLLESGSEVKKPGSSVKVSCRASGSSFRSYNFNWVPQAPGGGLEWMGGIIPM-FGTAN 59
                                                                                                                                 Score 605 DB 13; Length 129,
Pred. No. 3 186-40;
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                                                                                                                                                                        15; Mismatches 16; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24 MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LAKE, PHILIP
APPLICANT: LAKE, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VAPICELLA-ZOSTEP VIPUS
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                      MOLECULE TYPE: protein
SENCE 129 AA; 13930 MW; 96169 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08217918 Patent No. 5506132 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08217918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION NAME: Smith, Willaim M REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 Lytton Avenue
LENGTH: 129 amino acids
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                                STRANDEDNESS: single
TOPOLOGY linear
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                                                                                                                                 Query Match 63 8%,
Best Local Similarity 72 3%;
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                      120 GQGTLVTVSS 129
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                                                                                            SEQUENCE
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63.6%;

Best Local Similarity

Query Match

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80 ACKPÜGEVIISADASISIAYMELSSLPSDDTAMYYCAPDITAPGAAPIPLNFYGMDVWGQ 139
                              I EVQLLESGSEVKKPGSSVKVS/PASGGSFRSVNFNWVPQAPGGGJEWMGGIIPMFGIANY 60
20 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNFAISWVRQAPGGGLEWMGRIMPLFVTSTY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.7%; Score 595, DB 10; Length 102,
larity 82.5%; Pred No 2.146-39;
Conservative 12, Mismatches 5, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: William M. Smith
STREET: One Market Placa, Stewart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             102 AA.
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                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application PC/TUS9206185
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 55, Application PC/TUS9206185.
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SYSTEM: PC-DOS/MS-DOS
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SENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEFEPENCE/DOCKET NUMBER 114
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 87654
                                                                                                                                                                                                                                                                                             STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7
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STATE: California
COUNTRY: USA
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FILING DATE: 199108
CLASSIFICATION:
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GENERAL INFORMATION:
APPLICANT: Lonberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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Matches 80, Conserv
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PCT-US92-06185-55
                                                                                                                                                                 140 GITVIVSS 147
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                                                                                                                                                                                                           119 GTLVIVSS 126
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SEQUENCE
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                    APPLICANT: Lonberg, Nils
APPLICANT: Ray, Robert M
TITLE OF INVENTION: Transqenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 595; DB 7; Length 102; Pred. No. 2.14e-39; 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                 SSEE: Townsend and Townsend Rhourie and Crew F: One Market Plaza, Steuart Tower, Suite 200 San Francisco California
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1 0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: CAPP-1943
CLASSIFICATION: 800
                                                   102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCA 101
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61 AOKFOGRVIITADESTATGYMELSSLRSEDTAVYYCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA -
APPLICATION NUMBER: US 07,090,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA -
                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/853,408
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: TRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SEQUENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                          Sequence 63, Application US/08053131 Patent No. 5661016 GENERAL INFORMATION:
                                                                                                                                  Sequence 63, Application US/08053131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30,223
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TELECOMMUNICATION INFORMATION -
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-1991
                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Smith, William M. PEGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHAPACTEPISTICS:
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Best Local Similarity 82.58:
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READARLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                  US-08-053-131-63
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STATE:
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5 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVPQAPGQGLEWMGP1IP1LG1ANY 64
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Pred. No. 2.14e-39;
12; Mismatches 5; Indels
                                                                                                                                                                                                                         APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
CORPESPONDENCES: 152
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Polease #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: PRILING DATE: PYL/USYZ/lu983 FILING DATE: 19921217 CLASSIFICATION:
102 AA
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PHT.
                                                                                                                                                                              63, Application PC/TUS9210983 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-E0S/MS-DOS
                                                                                                                                     Seguence 63, Application PC/THS9210983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
JENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 55, Application US/U7834539A Patent No. 563342
GENERAL INFORMATION:
APPLICANT: Lonborg, Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 55, Application US/07834539A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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INFORMATION FOR SEQ 1D NO: 63:
SEQUENCE CHAPACTERISTICS:
STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTOPNEY/AGENT INFOPMATION:
NAME: Smith, William M.
PEGISTRATION NUMBER: 20.3
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AMINO ACID
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Best Local Similarity 82.5%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
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MEDIUM TYPE: Floppy
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PCT-11592-10983-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94105
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                                                                                                                                                                                   Sequence 63,
                                                                                           01-JAN-1900
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APPLICANT: Kay, Robert M.

TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
CORRESPONDENCES: 77

CORRESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                 5 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CO, Man Sung
APPLICANT: SCHEEIDEN, Milliam P.
APPLICANT: CONTENEDEN, Milliam P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, HARPOVER HYMANIZED IMMINYSLORIINS
NUMBER OF SEQUENCES: 113
                                                ADDRESSEE: William M. Smith
STREET One Market Plaza, Stenart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                       Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto
                                                                                                              COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: TRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pa-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred No 2 14e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCA 101
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                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                        FILING DATE. 1992026
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REPERBIOE/DOCKET NUMBER: 14643-5
TELECHONE: 415-543-9600
TELEPHONE: 415-543-9600
                                                                                                                                                                               APPLICATION NUMBER: US/07/834,539A FILING DATE: 19920205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPT:
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
SEQUENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08474040 Patent No. 5593761 GENERAL INFORMATION: APPLICANT: QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/08474040
                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHAPACTEPISTICS
                                                                                                                                                                                                                                                                                                               · 102 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDAPD;
                                                                                                                                                                                                                                                                                                                                    single
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                                                                                             USA
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                                                                                             COUNTRY:
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                                                                                                 MEDIUM TYPE: FIPPRY disk
COMPUTER: IBM PC COMPATIBLE
COURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474.040
FILING DATE: 07-010-1995
APPLICATION NUMBER: US 07/534,278
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,278
FILING DATE: 19-5EP-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-5EP-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTONENEY/ASBNIT NUMBER: US 07/290,975
ATTONENEY/ASBNIT NUMBER: US 07/290,975
ATTONEY/ASBNIT NUMBER: US 07/290,975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, William M
REGISTRATION NUMBER: 30,223
PERFPENCKET NUMBEP: 11823-002500
TELECOMMUNICATION INFORMATION:
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Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, CATY L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1.117
OTHER INFORMATION: /note= "Eu h
UTHER INFORMATION: sequence."
NCE 117 AA, 12472 MM, 77871 CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 104, Application US/08477728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEC 11 0. 15.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 79.0%;
Matches 79, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
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                                                     94301
                            COUNTRY:
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STATE:
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TELEPHONE: (415) 326-2400
TELEFAX. (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
APPLICANT: SELICK, HAROLG E.
TITLE OF INVENTION: IMPROVED
                                                                                                                                                                                                                                                                                                                                                                                                         117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                      113
                                                                                                                                                                                                                                                                                                                         Smith, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                             : protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 79.0%;
Matches 79; Conservative
                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                      NUMBER OF SEQUENCES:
                                                  STREET: Two Embarc
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: un
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-477-728-15
                                                                                          94111
                                                                                                                                          SOFTWARE:
                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 591; DB 6; Length 117; Pred. No. 4.58e-39;
     TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGLOBLINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches 10; Indels
                                                                                                            MEDLUM ILE: LINES COMPUTED COMPUTED IEM PC-DOS/MS-DOS SOPTWARE: Patentin Release #1.0, Version #1.25 SOPTWARE: PAPLICATION DAIR: APPLICATION NUMBER: US/08/477,728 FILING DAIE: 07-JUN-1995 CLASSIFICATION: 424
                                 : Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCAGGY 100
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                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                     FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
JENCE 117 AA; 12472 MW; 77871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08477728.
                                                                                                                                                                                                                                                                                                                    NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 104
                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                   117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.3%;
Best Local Similarity 79.0%;
Matches 79; Conservative
                NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                        Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                     94111
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                                     ADDRESSEE:
                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                             STREET:
                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1900
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ID US
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1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY 60
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LOCATION: 1.117
OTHER INFORMATION: /note= "Variable region of the human
OTHER INFORMATION: Es antibody heavy chain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 591; DB 6; Length 117;
Pred. No. 4.58e-39;
IMPROVED HUMANIZED IMMUNOGLOBLINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches 10; Indels
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                                               CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AQKFQGRVIITADESTNTAYMELSSLRSEDTAFYFCAGGY 100
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                                                                                               Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-UN-1956
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 77310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 77310,252
FILING DATE: 28-DEC-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             SOFTWARD. CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASCIFICATION: 424
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                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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05-08-477-728-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..117
OTHER INFORMATION: /note= "Eu heavy chain amino acid
                  Sequence 15, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: GUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TILLE OF INVENTION: IMPROVED HUMANIZED IMMUNGLOBLINS
NOMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA
FILING DATE: 07-UN-1995
                                                                                                                                                      E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.3%; Score 591; DB 6; 1
Best Local Similarity 79 0%; Pred No 4 5%-39;
Matches 79; Conservative 11; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFFCATION '424
PRODE APPLICATION OATA'
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA'
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NATA'
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290.975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
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Sequence 15, Application US/08477728
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                               CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                  STREET
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1 QVQLVQSGAEVKKPGSSVKVSCKASGGIFSFSAIIWVFQAPGQGLEWMGGIVPMFGPPNY 60
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                                                                                                                                                                                                                                                              APPLICANT: QUEEN, Cary L.
APPLICANT: QUEEN, GARY L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Hazold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMINOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.3%; Score 591; DB 6; Length 117; Best Local Similarity 79.0%; Pred. No. 4.58e-39; Matches 79; Conservative 11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Pelease #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor
117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Smith, William M
FEGISTRATION UNBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-UN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/319,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFFLICATION NUMBER US 07/410,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTOREY/AGENT INFORMATION:
PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE, peptide
JENCE 117 AA: 12472 MW; 77971 CN;
                                                                                                                                                                                          Sequence 72, Application US/08477728
Patent No. 585608
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
                                                                                                                                              Sequence 72, Application US/08477728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 amino acids
STANDARD;
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STATE: California
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ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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1 EVOLLESGSEVKKPGSSVKVSCPASGGSFPSYNFNWVPQAPGGGLEWMGGTIPMFGTANY 60
                                          61 AQKFQGRVIITADESTNTAYMELSSLRSEDTAFYFCAGGY 100
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                                                                                                                                         RESULT
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OTHER INFORMATION: /note= "Eu heavy chain amino acid
OTHER INFORMATION: sequence."
NCE 117 AA: 12472 MW: 77871 CN:
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBELINS NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 591; DB 6; Length 117;
Pred. No. 4.58e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-Dos/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/634,278
FILIG DATE: 19-DEC-1990
CLASSIFICATION: 424
                       117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION 10424
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
PPLIOR DATE: 13-FEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                       PRT;
                                                                                                                                                                                                Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: CO. Man Sund
APPLICANT: CO. Man Sund
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLEI, Nicholas
APPLICANT: COELINGH, Kathleen L.
                                                                                                                                                                                 Sequence 15, Application US/07634278
                                                                                                                                           Sequence 15, Application US/07634278.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                             SELICK, Harold E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, William M
REGISTRATION NUMBER: 30
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                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER PEADABLE FORM-MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palo Alto
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE PY
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
  LT 14
US-07-634-278-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY:
STATE:
                                                                                                   01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                               XXXXXX
  RESULT
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3 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAFGGGLEWMGGIVPMFGPNY 60

q

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/note= "Variable region of the human
En antibedy beary chain."
                                                                                                                                                                                                                                                                            TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOCLOBILINS NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: FEACH disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-LOSS/MS-DOS
SCPTAMES: Patentin Pc-LoSS/MS-DOS
SCPTAMES: Patentin NoTA:
APPLICATION NOMBER: US/07/634,278
FILING DATE: US/07/634,278
PRIOR APPLICATION: 424
PRIOR APPLICATION NOMBER: US/07/634,278
FILING DATE: L8-SEP-1990
PRIOR APPLICATION NOMBER: US/07/590,274
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NOMBER: US/07/690,975
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NOMBER: US/07/690,975
FILING DATE: R8-DEC-1988
APPLICATION NUMBER: US/07/690,975
FILING DATE: R8-DEC-1988
APPLICATION NUMBER: US/07/690,975
FILING DATE: US/07/07/100:
                                                                                                                                                                                                                                                                                                                      11 Townsend and Townsend Khourie and Crew 379 Lytton Avenue
61 AOKFOGRVTITADESTATGYMELSSLRSEDTAVYYCAMPY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/POCKET NUMBER 11823-002500
IELECOMMUNICATION INFORMATION:
                                                      PRT;
                                                                                                                                                                                                             CO., Man Sung
SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINE, Katcheen L.
SFLICK, Harold E.
                                                                                                                                                          Sequence 4, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary I..
                                                                                                                                  Sequence 4, Application US/07634278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEO 1D NO: 4:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, William M
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein LOCATION: 1.117 OTHER INFORMATION: CTUPE INFORMATION:
                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
STREET: 37
                                                                                                                                                                                                                                                                                                                                                                                      94301
                                                     US-07-634-278-4
                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                         01-JAN-1900
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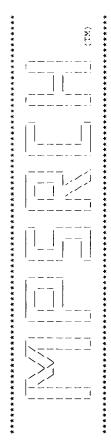
SQ SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 62.3%; Score 591; DB 6; Length 117; Best Local Similarity 79.0%; Pred. No. 4.58e-39; Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps

0;

QQ ò

Search completed: Tue Feb 24 07:42:57 1998 Job time : 14 secs.



Release 2 1D John F Collins, Riocomputing Pescarch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07.16:36 1999, MasPar time 10.72 Seconds 163.248 Million cell updates/sec Pun on:

Fabular output not generated

>US-08-844-215-7 (1-126) from US08844215 pep 949 1 EVQLLESGSEVKKPGSSVKV... Description: Perfect Score: Sequence:

...GSCWGWFDPWGQGTLVTVSS 126

PAM 150 Scoring table: 111726 seqs, 13889129 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq30

lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 3:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23

Mean 30 601; Variance 151.366; scale 0.202 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Query Match Length DB	DB	QI	Description	Pred. No.
1	773	81.5	481	Ŋ	R24442	Sequence of antibody	2.26e-54
CI	678	71.4	۲۰ ۲۰	œ	F31023	Antibody D heary chai	2 520-46
m	635	6.99	120	σ.	P54796	MpI evi	1.07e-42
4	634	66.8	123	C1	W19887	specific	1.30e-42
2	629	55.3	96	C 1	R72058	eqion.	3.43e-42
9	621	65.4	123	(1)	W19838	ā	1.62e-41
7	620	65.3	123	۲. د.	W19885	specific	1.97e-41
6 0	618	65 1	4.01	۳. ۲	м19899	CEA-specific antibody	14-00b 2
6	617	وي ن	.23	۲,	W19881	ر.	3.526-41
10	604		147	15	P65019	٧.	4.366-40
11	603	63.5	249	14	R77510	Humanised 5G1.1 VH +	5.30e-40
12	598	ω.	ч	53	W13536	Anti-melanoma antibod	1.390-39
13	595	C 4	86	~	P72059	HV1263 VH region.	2.496-29
14	595		117		R38623	Human heavy chain V r	m
15	595	62.7	117		R22358	Protein encoded by th	m
16	595	62.7	117	20	W03950	DNA fragment vh49.8,	\sim
	592	62.4	249	14	R77615	Humanised 5G1.1 VH +	4.45e-39
	591		•	C3	P24104	Human antibody Eu hea	œ.
19	265	62.3	۲. ر در	u:	R28742	Heavy chain variable	5.400-39
	587	61.9		14	P76954	HSV-neutralising anti	1.170-38

1116.25.00 - 1.0	.02e-3 .02e-3 .24e-3 .67e-3 .24e-3
Hy region of human rh Humanised CDP-grafted SpA-reactive 1gK heav Monoclonal antibody 5 Humanised CDR-grafted Humanised CGI.1 VH + Heavy chain variable Humanised CGI 1g hea Humanised CGI 1g heavy chain variable pro-ras humanised hoa Humanised mouse DRG-2 INPEG-200 Humanized an Humanised an Humanised an Humania nati-turour antiper Pro-ras anti-turour antiper Human anti-turour antiper Pro-ras Humanized an Humanian anti-turour antiper Paper Pro-ras Allenania antiper Pro-ras Allenania antiper Pro-ras Allenania Alle	manized VLA-4 ant manised alpha-4; neclosal antibody lated human Vii 9 1748RHB VH region avy chain variabl imeric anti HIV a manised heavy cha avy chain variabl
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ALIGNMENTS

PESTILT	F.
ΩI	R24442 standard; Protein; 481 AA.
AC .	0
DI Ed	02-JAN-1992 (first entry)
) Z	immunoslobulin G1.
SO	Homo sapiens.
FH	Key Location/Qualifiers
FT	ference
Ē.	Z
FI T	
Η̈́	Misc_difference 310
FI	
FJ	
FI	Misc_difference 321
FT	/label= N
FT	/note= "see above"
FT	Misc_difference 329
FT	/label= N
ΕI	/note= "see above"
ΕΞ	Misc_difference 331
FI	/label= s
БŢ	/note= "see above"
브	Misc_difference 356
FT	/label= N
E +	
E.	Misc_difference 369
FT	/label= N
드	/note= "see above"
Z.	WO9209293-A.
PD	
F)	18-NOV-1991; U08605.
4	23.NOV-1990, US-618314.
ΡA	CEN P
Id	m
D.F.	WPI; 92-215789/26.
S. H.	
ΡŢ	tion of cell adhesion mediated through ELAM-1
ЬŢ	- used in treating chronic inflammation, rheumatoid arthritis,
ΡŢ	
PS	losure; Fig 1; 46pp; English.
ဥ	form, bears no sialy1-Lex side cha
S S	scule including
رن ن	obains (se

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61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSPGSCW-GWFDPWGQG 119
                                                                                                                                                                                                                                                         85 aqkfqgrvtitadeststaymelsslrsedtavyycardngaycsgqscysgwfdpwggg 144
additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding ability. They are preferably located in the CH2 region of the Ty molecula. Antibodies bearing multiple sially-lax determinants are useful for disrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for
                                                                                                                                                                                                  25 qvqlvqsgaevkkpgssvkvsckasggtfssyaiswvrqapgqglewmggiiplfgtany 84
                                                                                                                                      Score 773, DB 5, Length 481;
Pred No 2 260-54;
11; Mismatches 10; Indels 1; Gaps
                                                                                                                                                                                                                             1 EVQLLESGSEVKKPGSSVKVSCPASGGSFPSYNFNWVRQAPGGGLFWMGGITPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heavy; light, chain, antibody, D, monoclonal, peripheral, blood, lymphocyte; hepatitis A virus; HAV; sero; positive; patient; murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodn. of recombinant primate antibodies - useful for treating infections caused by hepatitis A, B and C, herpes, cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
                                                                                        example, in minimising inflammation following tissue injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           R31023 standard; Protein; 476 AA.
                                                                                                                                      Query Match 81.5%;
Best Local Similarity 82.7%.
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WELL ) WELLCOME FOUND LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122..132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide 1..19
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85..113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUL-1992; 306420
15-JUL-1991; GB-015284.
01-AUG-1991; GB-016594
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody D heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50..54
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WPI; 93-019951/03.
                                                                                                                                                                                                                                                                                                                    145 tlvtvss 151
                                                                                                                                                                                                                                                                                                                                                120 TLVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q35099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- HINGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
/label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label - CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= FR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JAN-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- CH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- CH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            R31023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
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arthritis etc.
Disclosure: Fig 2: 35pp; English.
Disclosure: Fig 2: 35pp; English.
The sequences given in P31023 24 represent the beavy and light chains of Antibody D respectively Antibody D is a monocloual antibody which was derived from pertipheral blood lymphocytes from a hepatitis A virus (BAV) sero positive patient. Antibody D is closely related in nature to murine antibody B5B3. Total RNA was isolated from antibody D expressing cells and polyadenylated RNA was extracted. These polya RNA's were used to prepare a cDNA library which was screened for human kappa light (L) chains and two positive clones were detected.
Further heavy (H) chain closes were also isolated.
Sequence 476 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 sqnfqurvtitadkststahmeltsIrsedtavyycatdryrqanfdrarv qwfdpwqq 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stimulating prodn. of variable region gene family restricted antibodies. - through B cell super-antigen vaccination bischosure; Page 78; 130pp; English.

A B-cell superantigen (SAg) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The SAg is used to enhance production of VH, especially variable from 10 VH, especially VH, restricted Ass Touring attempts to identify SAgs, as sequences (ES484-80) of H chains from 19 reactive with mod-SpA, and as and DNA sequences (ES484-25), vol442-55) of VH regions of SpA binders obtained from combinatorial libraries were determined. IgM protein KAS is derived from the germline configuration of a VH quen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 qkfqqrrtitadestntaymelrslrsddtamyycakeqyqdy-qr-p-fd-f--wqqqf ll4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ÖKFÖGKVITTADESTATGYMELSSLESEDTAVYYCAMP-YPKHOSEGSKOWGWPDPWGGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                     20 gmgvygsgaevkkpgssvtvsckasggtfsnyaiswyrgapggalewmggiipliatpty 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l vhlygegjovkkpgssvkysckagagifssjalswyrgaljgglewmggiipitaganya 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VQTLESGSEVKKPGSSVKVSGPASGGSFRSYNFNWVRQAPGQGLEWMGGTIPMFGTANYA 61
                                                                                                                                                                                                                                                                                                                                                    sdro :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-0cT-1994 (first entry)
SpA-reactive IqM heavy chain clone KAS.
SpA domain D: Iq binding region; IqM; B-cell superantiqeu; SAq;
Superantiqen; heavy chain variable region; VH3 restricted antibody;
VH; protein-A; KAS; B-lymphocyte; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                               Match 71.4%; Score 678; DB 6; Longth 476; Local Similarity 71.1%, Pred. No. 2 520-46; es 91: Conservative on Mil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 635; DB 9; Length 120; Pred. No. 1.07e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 11; Indels
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Matches 97, Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-0CT-1992: US-969936.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1994.
29-0CT-1993; U10555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 qtlvtvss 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 GTLVTVSS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                       Query Match
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26-SEP-1995
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The sequences from CEA1-7 (see W19876-95) obtained by mutagenests or chain shuffling. (A) is used to detect cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 aqkfqgrltitadeststaymelsslrsedtavyyca-q-anscnrsyyy-ymdvrgqgt 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 qvqlvqsqaevkkpqssvkvsckasgqtfsnspinwlrqapqqqlewmgsiipsfgtany 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 12; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutagenesis or chain shuffling. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 634; DB 23; Length 123;
Pred. No. 1.30e-42;
                                                                                                                                         tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
Chimeric Homo sapiens;
                                                                                                            CEA-specific antibody CEÁ6 VH mutant HBAll sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
                                                                                                                                                                                                                                          /note= "complementarity determining region 1"
Region 50 66
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Peaton
                                                                                                                                                                                                                                                                                                                                   "complementarity determining region 3"
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                                                                                                                                                                                                   Location/Qualifiers
                                                      T 4
W19887 standard; Protein; 123 AA.
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Best Local Similarity 73.0%;
                                                                                              07-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allen DJ, McCafferty JG,
WPI; 97-319779/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        11-00T-1996; GR-021295
07-DEC-1995; GR-025004
23-MAY-1996; GR-010824
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                                                                                                                                                                                   Chimeric synthetic.
            121 LVTVSS 126
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                                                                                                                                                                                                                            /label= CDR1
                                                                                                                                                                                                                                                                       /label- CDR2
                                                                                                                                                                                                                                                                                                                   /label- CDR3
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                                                                                  W19887;
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1 qvqlvqsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtany 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (1961) genes showed homology to the closest germline genes. DP10 (200327) and hv1263 (200328). The DNA (200329) and corresp. amino acid hv1263 (200328). The DNA (200329) and corresp. amino acid DF731.2, are provided.
                                                                                                                                                                                                                                                                                                                                                                                               Graves' ophthalmopathy-associated monocional antibody - produced by molecular oloning of immunoglobulin genes by PCR Disclosure; Page 68: 94pp, English.

L- and H-chain DNA was amplifted by PCR from Graves' orbital
                                     Graves opithalmopathy associated immunoglobulin protein: orbital antigon; monoclonal antibody; heavy chain; H chain; variable region, autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 65.3%; Score 529; DB 12; Length 98; Local Similarity 86.6%; Pred. No. 3.43e-42; nes 84; Conservative 11; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carcinoembryonic antigen; CEA; human; antibody; scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
adenocarcinoma; diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEA-specific antibody CEA6 VH mutant HBB11 sequence.
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07-DEC-1995; GB-025004.

23-MAY-1996; GB-010824.

(CAME.) CAMBRIDGE ANTIROPY TECHNOLOGY.
Allen DJ, McCafferty JG, Osbourn JK.
                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                    22-SEP-1994; U10756.
22-SEP-1993; US-124469.
(NICH-) NICHOLS INST DIAGNOSTICS.
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W19888 standard; Protein; 123 AA.
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(first entry)
                                                                                                                                                                                                                                                                                                                                    Rapoport B;
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09-DEC-1996; G03043.
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                                                                                                                                                                                                                                                                                                                                  Mclachian SM, Rap
WPI; 95-139383/18.
                     DP10 VH region.
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WO9720932-A1.
                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; 08932
                                                                                                                                                                                                           /label= CDR2
                                                                                                                                                                    /label= CDR1
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This polypeptide sequence comprises the heavy chain variable region (VH), HBB1, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCBA)-specific antibody CEA6 (see W1981). A claimed specific binding member (A) comprises an hCBA specific antibody antigen binding domain that has a dissociation constant for hCBA of less than 1 x 10 - 8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 cextracellular domain of hCBA and/or to cell-associated hCBA over hCBA over soluble hCBA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. An example of a claimed pairing is HBB11 VH with CEA6 VL. (A) is used to detect cells expressing hCBA, in vivo or in vitro, especially tumour cells for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 aqkfqgrltitadeststaymelsslrsedtavyycar-h-nh-nyelyyyymdvwgqgt 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKFQGRVIITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSCWGWFDPWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 qvqlvqsgaevkkpgssvkvsckasggtfsnspinwlrqapgqglewmgsiipsfgtany 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
                      Specific binding members for human carcinoembryonic antigen - bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Specific binding members for human carcinoembryonic antigen - bind
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                                     to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.4%; Score 621; DB 23; Length 123; Best Local Similarity 73.0%; Pred. No. 1.62e-41; Matches 92; Conservative 16; Mismatches 15; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                               adenocarcinoma of the colon, lung or breast.
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CEA-specific antibody CEA6 VH mutant TO6D10 sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
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Region 99..112
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                                                                                                 Claim 4; Fig 2; 128pp; English.
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11-OCT-1996; GB-021295.
07-DEC-1995; GB-025004.
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Chimeric synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                123 AA;
WPI: 97-319779/29
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                                                                                                                                                                                                                                                                                                                                                                                             cancer, e.g.
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61 agkfggrltitadeststaymelsslrsedtavyyca-gcshnyel-yyy-ymdvwqqqt 117
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            This polypeptide seguence comprises the heavy chain variable region (VH), ToSD10, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (htch3-specific antibody CEA6 (see https://www.ybsul.ac.antigen binding member (A) comprises an horax specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferred in the call of the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) chrained by mutagenesis or chain shuffling. Examples of claimed pairings are TOSD10 VH with TOSD12 or CEA6 VL. (A) is used to detect cells.
                                                                                                                                                                                                                                                                expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing canner, e.g. adenorarcinoma of the colon, lung or breast Sequence. 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                            3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide sequence comprises the heavy chain variable region (VH), HBBG. obtained by mutagenesis of the VH CDR3 of human carcinocembryonic antigen (hDEA) specific antibody CEA6 (see W19881). A claimed specific binding member (A) comprises an hCEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Specific binding members for human carcinoembryonic antigen - bind
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                                                                                                                                                                                                                                                                                                                                                 Match 55.3%; Score 620; DB 23; Length 123; Local Similarity 72.2%; Pred. No. 1.97e-41; es 91; Conservative 16; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
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CEA-specific antibody CEA6 VH mutant HBB6 sequence.
Carchoembryonic antiqen; CEA; humani antibody; sefv:
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Region 50..66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osbourn JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     л 8
W19889 standard; Protein; 123 AA.
Claim 4; Fig 2; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 2; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCafferty JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31..35
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07-DEC-1995; GB-025004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric Homo sapiens;
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-1996; GB-010824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-DEC-1996; G03043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 mvtvss 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen DJ,
                                                                                                                                                                                                                                                                                                                                                     Query Match
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1 qvqlvqsgaevkkpgssvkvsckasggtfsnspinwlrqapgqglewmgsiipsfgtany 60
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This polypeptide sequence comprises the heavy chain variable region (WH) of human carcinoembryonic antigen (hCEA)-specific antibody CEA6. W (77215-32) and VL (772133-35) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see W19876-85).

A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 - 8 M, is non-cross-reactive with human diver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA cver
                                                                                                                                                                                                                                                                                                          3, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells, used for diagnosing
                constant for NCEA of less than 1 x 10 -8 M. In more constant to the A3-B3 with human liver cells, and preferentially binds to the A3-B3 vertacellular domain of http and/or to cell associated http Aver http Aver block over soluble http. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. An example of a claimed pairing is HBB6 VH with CEA6 VL. (A) is used to detect cells expressing http. An example of a claimed pairing is HBB6 VH with CEA6 VL. (A) is used to detect cells for diagnosing
      specific antibody antigen binding domain that has a dissociation
                                                                                                                                                                                                                                                                Ouery Match 65.1%: Score 618; DB 23; Leugth 123; Best Local Similarity 73 0%; Pred. No. 2 90e-41; Matches 92; Conservative 15; Mismatches 16, Indels
                                                                                                                                                                                                       cancer, e.g. adenocarcinoma of the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEA-specific antibody CEÁ6 VH sequence.
Carcinoembryonic antigen; CEA, human, antibody, scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "complementarity determining region 1" Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenocarcinoma; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1-OCT-1996; GB-021295.
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23-MAY-1996; GB-010824
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09-DEC-1996; G03043
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                                                                                                                                                                                                                          123 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CDR2
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                                                                                                                                                                                                                              Sequence
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Claim 8. Fig 48; 39pp. English.

A human anti-Varicella zoster virus monoclonal antibody was prepd.

S human anti-Varicella zoster virus monoclonal antibody was prepd.

S proposed to the professor of complement.

This cell line, designated cell line TC93KA9, produced an antibody designated 93KA9 entibody were cloned using PCR. At least two genes of the 93KA9 antibody were cloned using PCR. At least two meavy chain (gamma-1) and two light chain (kappa) specific clones were sequenced (see Q82749 & Q82750 respectively).
                                                                                                                                                                                                                                                                                            61 aqkfqgrltitadeststaymelsslrsedtavyycagr-shnyel-yyy-ymdvwgqgt 117
                                                                                                                                                                                                                       Score 617; DB 23; Length 123;
Pred. No. 3.52e-41;
16; Mismatches 16, Indels 3; Gaps
            sequences from CEA1-7, or their CDR sequences, as well as CEA6 Wh with W and VL variants, including combinations of CEA6 VH with VL regions from CEA6, TCSA4, TC56D12, LCBIC, LCBIC or LCSC2.

(A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma sequence 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Varicella zoster virus; VZW: anti-VZW monoclonal antibody; 93KA9; 91ycoprotein II subunit; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1995 (first entry)
93RA9 anti-Varicella zoster virus antibody heavy chain variable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human monoclonal antibodies specific for the glyco:protein II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - used in a therapy and
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soluble hCEA. Preferred (A) include pairings of VH and VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region 50..54
Tabel= complementarity determining region (CDR) Region (CDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key Location/Qualifiers
Protein 20..147
/label= mature light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sub:unit of varicella zoster virus prophylaxis of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R65019 standard; Protein; 147 AA.
                                                                                                                                                      65.08;
                                                                                                                                                                    Best Local Similarity 72.2%;
Matches 91, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1993; US-098479.
24-MAR-1994; US-217918.
(SANO ) SANDOZ PHARM CORP.
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N-PSDB: 082750.
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                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
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20 qvqlvqsgaevkkpgssvkvsckasggtfsnfaiswvrqapgqglewmgrimplfvtsty 79

Matches

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Best

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis Example 11: page 119-122; 181pp: English.

A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH + IGHRL (R77610), includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. It can be co-expressed with a humanised light chain (R77612) in human 293 BDNA cells using encoding DNAs subcloned into vector APBX.3P (T08476). Such humanised recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSCWGWFDPWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 aqkfqgrvtmtadtststaymelsslrsedtavyycar-yf-fgsspn-w-yfdvwgqgt 135
                                                   61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSCWGWF--DPWGQ 118
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1 EVQLLESGSEVKKPGSSVKVSCRASGSFRSYNFNWVRQAPGQGLEWMGGIIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                           80 aqkfqgrvtısadaststaymelsslrsddtamyycarditapgaaptplnfygmdvwgq
                                                                                                                                                                                   15-MAR-1996 (first entry)
Humanised SG1.1 VH + IGHRL.
Complement C5; haemolysis: kidney: glomerulonephritis;
monoclonal antibody; antihnflammatory; antibody engineering;
humanised antibody; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 603; DB 14; Length 249;
Pred No 5 30e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Mismatches 17, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomas TC;
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                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
ID W13536 standard; protein; 119 AA.
                                                                                                                                                           R77610 standard; Protein; 249 AA.
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70.6%;
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                                                                                                                                                                                                                                                                                                                                                                                   118..130
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02-MAY-1994; US-236208.
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Best Local Similarity
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                                                                                140 gttvtvss 147
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                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                         R77610;
                                                                                                                                                                                                                                                                               Peptide
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From a cancer patient.

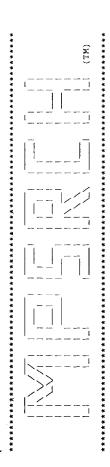
PS A process for isolating and synthesising human monoclonal anti-tumour cancers for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at antibodies has been produced. The process involves: (a) constructing at antibodies has been phage library from the peripheral blood lymphocytes.

(PBLS) of a cancer patient; (b) screening for anti-tumour antibodies in the phage is the patient; (c) screening for anti-tumour antibodies in the phage is the patient; (c) assay with cultured tumour cells of the absorption against normal human cells; (d) cloning the phage by coupacting the phage with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phage by coupacting the phage with at least two types of cultured normal cells; coupacting the phage with a least two types of cultured normal cells; coupacting the phage for more than one other tumour that is not the patient's tumour. The present sequence represents a human heavy a method as described and very antibody fusion phage library, produced by a method as described and therapeutic applications and for isolating tumour constitutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigens for studying tumourigenesis or for use as anti-cancer vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MADS). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a tumour cell line can be improved by genetic manipulations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 rvtitadkststaymelsslrsedtavyyca---r--g-ggrydafdiwqqqtlvtvss 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 gglevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtanyaqkfgg 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Gaps
28-OCT-1997 (first entry)
Ant: melanoma antibody 2-71 from VH antibody fusion phage library.
Human; monoclonal antitumour antibody; peripheral blood lymphocyte; cancer; tumouriqenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                    Prodn. of human monoclonal anti-tumour antibodies - by screening a
                                                                                                                                                                                                                                                                                                                                             usion phage library produced using peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen; monoclonal antibody; heavy chain; H chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graves ophthalmopathy associated immunoglobulin protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 598; DB 23; Lenc
--- No. 1.39e-39;
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(NICH-) NICHOIS INST DIAGNOSTICS.
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R72069 standard; Protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 63.0%;
Local Similarity 77.5%;
les 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rapoport B;
                                                                                                                                                                                                                    US-497647.
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                                                                                                                                                                                                                                                                                                                                                                                  from a cancer patient
                                                                                                                                                                                    28-JUN-1996; IB1032.
30-JUN-1995; US-49764
(UYYA.) UNIV YALE.
Cai X., Garen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-1994; U10756.
22-SEP-1993; US-1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA;
                                                                                                                                                                                                                                                                    Cai X, Garen ...
upr: 97-109061/10.
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                                                                                                                                          WO9702479-A2.
23-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Job time : 14 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 595; DB 7; Length 117;
Pred. No. 2.49e-39;
12; Mismatches 5; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 qvqlvqsgae::kkpgssvkvsckasggtfssyaiswvrqapgqglewmgriipilgiany 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLLESGSEVKKPGSSVKVSCRASGGSFRSYNFNWVRQAPGGGLEWMGGIIPMFGTANY 60
                                                                                                                                                                                                                                                              5; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A human placental genomic DNA library cloned into the phage vector manner for XI I was screened with the human VH1 family specific oligonucleotide Q44186 clone lambda 49 8 was isolated and a 6.1kb xbal fragment containing the variable segment VH49.8 was subcloned into pnv03 to generate plasmid pu49.8. An 800bp region of this insert was sequenced (Q44185) and VH49.8 found to have an open reading frame and intact splicing and recombination sequence Q44185 was deduced from the coding sequence; the last 3 codons before the termination codon have not been translated.
                                           by molecular cloning of immunoglobulin genes by PCR Disclosure; Page 69; 94pp; English.

Land H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (1gG1) genes showed homology to the closest germline genes, DPID (QR9377) and hv1263 (Q89389). The DNA (Q89329) and corresp. amino acid (R72070) sequences of the VW region of a representative clone, OP7H1.2, are provided.
               N-PSDB+ Q89328.
Graves' ophthalmopathy-associated monoclonal antibody - produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic non-human animals contg. immunoglobulin heavy chain trans gene - used to produce useful antibodies by isotype
                                                                                                                                                                                                                               Score 595; DB 12; Length 98;
Pred No. 2 496-39;
12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NoV-1993 (first entry)
Human heavy chain V region VH49.8.
Immunoglobulin, IgG; heavy chain; minilocus transgene;
Isocype switching; H chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 aqkfqgrvtitadkststaymelsslrsedtavyyca 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AQKEQGRVIITADESIATGYMELSSLRSEDIAVYYCA 97
                                                                                                                                                                                                                                                                                                                                                                   61 aqkfqgrvtitadkststaymelsslrsedtavyyca 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; Page 96; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R38623 standard; Protein; 117 AA
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                                                                                                                                                                                                                               Query Match 62.7%;
Best Local Similarity 82.5%;
Matches 80; Conservative
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17-DEC-1991; US-810279.
18-MAR-1992; US-853408.
23-UUN-1992; US-904068.
(GENP-) GENPHARM INT INC.
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nes 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 93-214169/26.
N-PSDB; Q44185.
95-139383/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA:
                                                                                                                                                                                               98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
WO9312227-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1993
                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R38623;
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20 qvqlvqsgaevkkpgssvkvsckasggtfssyaiswvrqapgqglewmgriipilgiany 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name of the control of the control of the coloques non-rearranged and/or rearranged in chains non-rearranged and/or rearranged in chains non-rearranged and/or rearranged in chains a care in the human placental genomic DNA library cloned into the phage. The human placental genomic DNA library cloned into the phage specific oligonucleotide (see 02418). Phage clone lambda 49.8 was isolated and a 6.1 kb xbai fragment contq. the variable segment VH49.8 subcloned into pNNN3 to generate plasmid pVH49.8 and 80.0 bp region of this insert was sequenced. VH49.8 was found to have an open reading frame which encoded the sequence shown.
                                                                                                                                  ω
                                                                                             17-AUG-1992 (first entry)
Protein encoded by the human heavy chain V region gene VH49.
Heavy chain; variable region; VH1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 % Match 62.7%; Score 595; DB 4; Length 117; Local Similarity 82 5%; prod No 2 496-39; nes 80; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 agkfggrvtitadkststaymelsslrsedtavyyca 116
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.I 15
R22358 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                      (GENP-) GENPHARM INT INC.
                                                                                                                                                                                                                                                          19-MAR-1992.
28-AUG-1991; U06185.
29-AUG-1990; US-574748.
31-AUG-1990; US-575962.
                                                                                                                                                                                                                                                                                                                                                                                                                           , Kay R,
13962/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PDSB; Q22419.
                                                                                                                                                                                                 Homo sapiens.
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Lonberg N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                      R22358;
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Release 2 1D John F. Collins, Biocomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 (7-17-55 1998; MasPar time 8 23 Seconds 466.347 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-844-215-6 (1-126) from (S08944215 pop 925 1 EVQLLESGPGLVKPSGTLSL.....RMMLDAFDIWGQGTLVIVSS 126 Description: Perfect Score:

Sedneuce:

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Tranni 2 acn2 3 ann3 4 ann4 5 unanni 6 unann2 7 unanni Biumann4 9 unanni 10 unann6 11 unanni 12 unann8 13 unann9 14 unanni0 15 unannii 16 unanni2 17 unann

Mean 41.798; Variance 118.726; scale 0.352 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	614	66.4	129	7	S44114	Iq heavy chain V red	3.47e-68
2	611	66.1	130	7	831690	heavy chain V	.32e-
m	608		134	7	S54906	G1 heavy chain	.51e-
4	598	64.6	86	7	S26905	Je.	-9 C
'n	598	•	98	7	S12419	Id heavy chain V red	6.750-66
9	597		139	7	S31586	heavy chain V	390-
7	588		123	^	S30529	heavy chain V	1.81e-64
œ	585		140	^	137782	variable regio	
6	583	63.0	96	7	S12417	Iq heavy chain v req	9.39e-64
10	583		ď	7	826904	heavy chain V	9.39.1-64
11	581		130	7	S30534	heavy chain V	1.81e-63
12	581	62.8	147	7	513519	heavy chain V	1.810-63
13	575		155	۲-	831512	heary chain -	1.30e.62
14	574		155	^	831511		1.80e-62
15	569		146	~	S09710		
16	267		86	7	S12413	heavy chain V	
17	567		98	7	\$26903	heavy chain v	1.79e-61
18	564		86	7	S12414	heavý chain V	4.80e-61
19	563	6.09	135	7	316	6	- 1
20	561		105	۲	4	a chain V	1 286-60

S31690 #type fragment
Ig heavy chain V region - human (fragment)
#formal_name Homo sapiens #common_name man

TITLE ORGANISM

RESULT ENTRY

60.6 137 7 831676 Ig heavy chain v 60.2 122 7 850312 13 heavy chain v 60.2 123 7 820532 13 heavy chain v 60.2 123 7 820532 13 heavy chain v 655 60.0 132 7 830911 13 heavy chain v 655 60.0 121 7 84413 13 heavy chain v 655 59.9 140 7 84413 13 heavy chain v 655 59.7 97 7 826905 13 heavy chain v 655 59.7 97 7 826905 13 heavy chain v 656 59.5 116 7 826902 13 heavy chain v 657 69.6 10 7 826902 13 heavy chain v 658 69.6 10 7 826902 13 heavy chain v 659 69.6 126 7 826902 13 heavy chain v 650 69.6 126 7 826902 13 heavy chain v 650 69.0 97 826892 13 heavy chain v 650 69.0 97 826892 13 heavy chain v 650 69.0 10 7 826892 13 heavy chain v 650 69.0 10 7 826892 13 heavy chain v 650 69.0 10 7 826892 13 heavy chain v 650 69.0 10 7 826892 13 heavy chain v 650 69.0 10 7 826802 13 heavy chain v 650 69.0 10 7 826802 13 heavy chain v 650 69.0 10 7 826802 13 heavy chain v 650 69.0 10 7 826802 13 heavy chain v 650 69.0 10 7 826802 13 heavy chain v 650 69.0 10 7 826802 13 heavy chain v 650 69.0 10 7 826802 13 heavy chain v 650 69.0 10 7 826802 13 heavy chain v 650	nission summitted to the RMEL bata in diotypic vaccination against of variable region gene seg assion S44114 preliminary single chain fv status status brained bua preliminary munoducule_type DNA status 1-129 ##label HAW stooss-references EMBL:231579 precidues 1-129 ##label HAW stooss-references EMBL:231579 precidues precident precident process and stooss-references EMBL:231579 precidues precident precid
22.22.22.22.22.22.22.22.22.22.22.22.22.	#access #access ##st ##st CLASSIFICA ##CI CLASSIFICA ##CI CLASSIFICA ##CI CLASSIFICA ##CI CUETY Ma Best Loc Matchos Db 11 CY 119 CY 119

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CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 134 #checksum 1180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                          Tonnelle, C. submitted to the EMBL Data Library, June 1992 submitted to the EMBL Data Library, June 1992 Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3, Gaps
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                                                                                   Cuisinier, A.M · Gauthier, L ; Boubli, L.; Fougerean, M
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Esposito, G.; Traboni, C. submitted to the EMBL Data Library, November 1994 Cloning and sequencing of cDNA coding for the variable domains of a human antibody against Hepatitis C virus
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#formal_name Homo sapiens #common_name man
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match

66.1%: Score 611; DB 7; Length 130
Best Local Similarity 73.2%; Pred. No. 9.32e-68;
Matches 93; Conservative 12; Mismatches 19, Indels
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##cross-references EMBL:X82935
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Matches 90; Conservative
                    16-Aug-1996
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The repertoire of human germline V(H) sequences reveals about fifty groups of V(H) segments with different hypervariable
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FICATION #superfamily immunoglobulin V region: immunoglobulin homelony
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FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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                                     Ig heavy chain V region (DP-70) - human (fragment)
#formal_name Homo sapiens #common_name man
22-Nov-1993 #sequence_revision 10-Nov 1995 #text_change
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Ig heavy chain V region (4.19) - human
#formal_name Homo saplens #common_name man
18-Feb-1994  #sequence_revision 10-Nov-1995  #text_change
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little polymorphism.
#cross-references MUID:90059975
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Pred. No. 6.75e-66;
....** has 7; Indels
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Ig heavy chain V region - human
*formal_name Homo sapiens *common_name man
06-Jan-1995 *sequence_revision 06-Jan-1995 #text_change
16-Aug-1996
                                                                                                         S31586 #type fragment
Ig heavy chain V region - human (fragment)
#formal_name Homo sapiens #common_name man
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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                                                                                                                                                                                                                                                        Tonnelle, C. submitted to the EMBL Data Library, June 1992 submitted to the \ensuremath{\mathsf{EMBL}}
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Pred. No. 1.81e-64;
12; Mismatches 21; Indels
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Local Similarity 73.0%; Pred. No. 9.39e-66;
les 92; Conservative 13; Mismatches 15.
                                61 NPSLNDPVFMSVDKSKDQVSLRLSSVTAADTAVYYCAP 98
51 npslksrvtisvdksknqfslklssvtaadtavyycar
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Best Local Similarity 71.0%;
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*superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M. Proc. Natl Acad Sci. II.S.A. (1994) 91:514-518
#title Somatic diversification in the heavy chain variable region genes expressed by human autoantibodies bearing a lupus-associated nephritogenic anti-DNA idiotype.
#accession 137782
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EMBO J. (1989) 8:3741-3748
                                                                                                                                                                                                                                                                                                                                         Ig variable region (VDJ) (clone T23-9) - human (fragment) #formal_name Homo sapiens #common_name man 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change
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Ig heavy chain V region (4.17) - human
#formal_name Homo sapiens #common_name man
18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
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#cross-references MUID:90059975
#accession S12417
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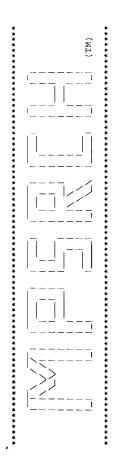
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FICATION *superfamily immunoglobulin homology
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FTSATION #superfamily immunoglobulin V region; immunoglobulin homology
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#formal_name Homo sapiens #common_name man
22.Nov-1993 #sequence_revision 10.Nov-1995 #text_change
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#formal_name Homo sapiens #common_name man
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
16-Aug-1996
#length 98 #molecular-weight 10634 #checksum 6422
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Best Local Similarity 81 6%;
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Best Local Similarity 81.6%,
Matches 80; Conservative
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##cross-references EMBL:X56158
FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                        61 ynps1ksrvtisvdtsknqfs1klssvtaadtavyycardkqqfwsgyytrnsruatdiw 120
                                                                                                                                                                                                                                                                                              60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNQG----RMMLDAFDIW 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $13519 *type complete
Ig heavy chain V region precursor - human
*formal_name man
2<-ppt-1994 *sequence_revision 10-Nov-1995 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mortari, F.; Ochs, H.D.; Wedgwood, P.1 P.; Schroeder Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Gaps
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#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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         DB 7; Length 130;
                                                               24; 104018
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                                 Pred. No 1 81e-63;
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                                                               ງດ; Misma⁺ຕho⊝
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Score 581;
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   Query Match 62.8%;
Best Local Similarity 70.8%;
Matches 92, Conservative
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Search completed: Tue Feb 24 07:14:17 1998
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                                                                                   *superfamily immunoglobulin V region; immunoglobulin homology
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Ig heavy chain V region - human
#formal_name Hn V capiens #common_name man
21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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1g heavy chain - human
*formal_name Homo sapiens *common_name man
13.Jan-1995 *sequence_revision 13-Jan-1995 *text_rhange
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                                                                                                                                                #domain immunoglobulin homology #label IMM #length 155 #molecular-weight 17235 #checksum
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Pred. No. 1.80e-62;
20; Mismatches 19; Indels
                                                                                                                                                                                                                                    Pred. No. 1.30e-62;
22; Mismatches 18; Indels
                                                                                                                                                                                                             Query Match 62.2%; Score 575; DB 7; Best Local Similarity 65.9%; Pred. No. 1.30e-62 Matches 83; Conservative 22; Mismatches 1
                                                                                                          heterotetramer; immunoglobulin
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                                                               ##cross-references EMBL:X69860
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preliminary
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Local Similarity 66.7%;
Les 84; Conservative
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*superfamily immunoglobulin V region; immunoglobulin homology
$69710
Hughes-Jones, N.C.: Bye, J.M.: Beale, D.; Coadwell, J.
Biochem. J. (1990) 268:135-140
Nucleotide sequences and three-dimensional modelling of the
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18; Mismatches 26; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                              #domain immunoglobulin homology #label IMM #length 146 #molecular-weight 16049 #checksum 2558
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Best Local Similarity 64.6%;
Matches 82; Conservative
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                               #authors
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       REFERENCE
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, H K Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:12:22 1998; MasPar time 5.58 Seconds 478.962 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-844-215-6 (1.126) from US08844215.pep 925 Description: Perfect Score:

1 EVQLLESGPGLVKPSGTLSL.....RMMLDAFDIWGQGTLVIVSS 126 Sequence:

Scoring table:

59021 segs, 21219398 residues PAM 150 Gap 11

Minimum Match 0% Listing first 45 summaries Post-processing:

Searched.

Database:

swiss-prot34
l.part1 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7
8.part8 9.part9 10.part10 11.part11

Mean 42 377; Variance 75 063; scale 0 565 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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### ALIGNMENTS

1 V2F_HTMAN STANDAP 01824;	21-7UL-1986 (PEL N, PEPATED) 21-7UL-1986 (PEL O1, LAST SECUENCE UPDATE) 21-JUL-1986 (PEL O1, LAST ANNOTATION UPDATE) 1G HEAVY CHAIN V-II REGION (WAH).	BUKAPYOTA: METAZOA; CHOPDATA; VEPTERPATA; TETPAPODA; MAMMALIA; BUTHERIA; PRIMATES. [1]		TAKAHASHI N. TETAPPI D., DEMIPDE B., LIN LC., PUTNAM F.W.; PROC. NATL. ACAD. SCI. 0.S.A. 79:2595-2584(1982). -1- THIS CHAIN WAS ISOLATED FROM AN IGD MYRLOMA PROPERN.	PIR: A02099; D2HUWA. HSSP; P01607; 1FGV. IMMUNOGLOBULIN V REGION.	NON_TER 129 129 SEQUENCE 129 AA; 14117 MW; 25BAB2F5 CRC32;	Query Match Best Local Similarity 62.5%; Pred No 1 00e-95; Matches 80, Conservative 20; Mismutches 25, Indels 3; Gaps 3;	2 lglgesgpglykpsetlsltcrysggprxrtgyywgwirgppgkglewiggyyrtgstyy 61	2 VOLLESGEGLVKPSGTLSLITTIVITY SCHWWSWVPTDPGKSLEWIGEVEFSGSTIY 60	62 npslrgrytisvdtsrngfslnlrsmsaadtamyycargnpppyydigtgsddgidvwgg 121	61 NPSENDPVEWSVDYSKEGVSERISSVTAACTAVYYARES-FIRMNG-GEMMEGAFITW3Q 118	122 gttyhvss 129	119 GTLVIVSS 126	C LI	HVILHUMAN STANDAFE; FPT, 145 AA. P06331;	01-JAN-1988 (REL. 06, CREATED) 01-JAN-1988 (REL. 05, LAS! SPAMENCE UPDATE) 01-NOV-1890 (PEL. 16, LAST ANNOTATION UPDATE) IG HEAVY CHAIN PRECURSOR V-II REGION (ARH-77)
RESULT ID H AC P	FT FT ES		RP RP	A H C	DR DR KW	FT S2	C B X	ac ac	Ωž	ac	27	십	ΩY	RESULT	AC AC	

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80 ktslksrvtisldtsknlfslklssvtaadtavyycargllrggwndydyyygmdvwggg 139
                                                                                                                                                                                                                                                                                                            1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWMSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                    20; Mismatches 28; Indels 2; Gaps
                                                                                                                              IG HEAVY CHAIN V-II REGION (ARH-77).
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA: TETRAPODA; MAMMALIA;
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                Score 512; DB 5; Length 146; Fred. No. 2.40e-87,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
MEDLINE: 78066916.
3. BIOL. CHEM. 253:586-597(1978).
1. THIS CHAIN WAS ISOLATED FROM AN IGGI MYELOMA PROTEIN.
PIR; A02100; GHUUM.
PIR; A02100; GHUUM.
IMMUNGLOBULIN V REGION: 3D-STRUCTUPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRPOLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLJAK R.J., NAKASHIMA Y., CHEN B.L., KONIGSBERG W.;
BIOCHEMISTRY 16:3412-3420(1977).
                                            MEDLINE; 85205332.
KUDO A., ISHIHARA T., NISHIMURA Y., WATANABE T.;
GENE 33:181189(1985).
PIR; A02101; GIHUH2.
HSSP: P01825; 1FGV.
                                                                                                                                                                                          72F1CBA8 CRC32,
                                                                                                                                                                                                                                                                                                                                                                                                                                 21-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-II REGION (NEWM).
                                                                                                                                                                                                                                                                                                                                                                                                          117 AA.
                                                                                                                                                                       BY SIMILARITY.
                                                                                                                                         SEGMENT.
                                                                                                                                                  D SEGMENT.
                                                                                                       IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                            16228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (REL. 01, CREATED)
                                                                                                                                                                                                              Query Match
Best Local Similarity 60.6%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                       117
127
146
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                          146 AA;
                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 77242302.
                                                                                                                                                                                                                                                                                                                                         140 ttvtvss 146
                                                                                                                                                                                                                                                                                                                                                             120 TLVIVSS 126
                                                                                                                                      20
118
128
42
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                                                                                                                                                                                                                                                                                                                                                                                                     HV2G_HUMAN
P01825;
                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
STRAND
                                                                                                                    SIGNAL
                                                                                                                                       DOMAIN
                                                                                                                                                  DOMAIN
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                                                                                                                                                            DOMAIN
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STRAND
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                                                                                                                                                                               1 EVQLLESGPGLVXPSGTLSLTCTVSGGSIPSSHWWSWVPQPPGKGLFWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Mismatches 20; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V REGION (M315).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK 2, COMPLEMENTABILY - DETERMINING 2.
                                                                                                                50.9%; Score 471; DB 5; Length 117; 66.3%; Pred. No. 4.03e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 440; DB 5; Length 116;
Pred. No. 3.39e-71;
                                                                                                                                      15; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        LERREQUE S.G., GEARHART P.J.,
                                                                                                                                                                                                  60 ttplrsrvtmlvdtsknqfslrlssvtaadtavyycarnli 100
                                                                                                                                                                                                              61 NPSLNDKVEMSVDKSKLQVSLRLSSVTAAD/TAVYYCARSP1 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 npslknrisitrdtsknqfflklnsvttedtatyycar 116
                                                                                             12790 MW; C5721B7B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13095 MW: 810F3E97 CRC32;
                                                                                                                                                                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NoV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE HPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                   116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                   01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDAT
01-NOV-1990 (REL. 16, LAST NONOTATION UPDAT
IG HEAVY CHAIN PRECURSOR V PEGION (M315).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK 3
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/CJ;
MEDLINE; 89279149.
LEVY N.S.; MALIPIERO U V., LEHROG, J. EXP. MED. 150-2007-2019(1989).
PIR; JT0509; HYMS31.
HSSP; P01825; LBAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                            Similarity 66.3%;
67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 59.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                   STANDARD;
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 63
66
72
76
82
89
98
107
115
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48
48
53
67
84
116
61
64
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77
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87
91
104
111 1
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85
40
116
116 AA;
                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        1LT 4
HV60_MOUSE
P18531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1LT 5
HV61_MOUSE
P18532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
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DISULFID
NON_TER
                                                                                             SEQUENCE
                                                                                                                  Query Match
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                                                   HELIX
STRAND
                     STRAND
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                                          STRAND
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HELIX
TURN
                                TURN
                                                                                                                                       Matches
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6.0 YNPSLNEPVEMSVLKSKELVSLFLSSVIAANTAVYYGARSPIKMN24PMML-DAFDIWGQ 118
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UNPUBLISHED RESULTS, CITED BY:
UNPUBLISHED RESULTS, CITED BY:
COLD SPRING HARB. SYMP CHANT. BICL 41:627-637 (1977).

--- THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS ANILL DINITROPHENT ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IC HEAVY CHAIN V PEGION (MOPC 315).
                                                                                                                                                                                                                                                                                       EUKAPYOTA; METAZOA; CHOPDATA; VERTERRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY - DETERMINING 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 45.1%; Score 4.77; 58.5; Length 137; Best Local Similarity 58.8%; Pred. No. 4.34e-66; Matches 57; Conservative 19; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTAPITY-DETERMINING
FRAMEWORK 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.

G -> GG (IN G295908).

G -> H (IN REF. 2).

GY -> YG (IN REF. 4).

N -> C (IN REF. 4).

MISSING (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE: 74170779.
FRANCIS S H., LESLIE P G Q , HOOD L , BISEN H.N.;
PROC NATL. ACAD. SCI. U.S A 71-1123-1127(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A. 74:5692-5696(1977).
                                                                                                                                                                                                                                                                                                                                                                             PINFPET A, HOPNE C., DOPPINGTON K 7, KLEIN M.; MOL. IMMUNOL. 26:431-434(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ZEMELL P., BUPSTEIN Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15399 MW; 155A5E8D CRC32;
                                                                                                                                                                                               21-JUL-1986 (REL. 01, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                      IG HEAVY CHAIN PRECURSOR V PEGION (MOPC 315).
MUS MUSCULUS (MOUSE)
                                                                                                                                                            137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPAMEWORK 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01789; 2FGW.
IMMUNOGLOBULIN V PEGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79148758.
* 1 , Wolf O , ZEMEIL )
3 38:1839-1845(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M27638; G603707; -...
EMBL; X07880; G295908; -...
PIR; PL0102; AVMS35.
HSSP; P01789; 2FGW.
                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE, 78094475.
JILKA R.L., PESTKA S.;
PROC. NAIL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448
544
1111
1114
1154
78
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123
137
137 AA;
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                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 77244979.
                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 89238351
PINFPET A , HOPNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-31
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85
85
40
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SCHECHTER I
                                                     140 gt 141
                                                                                         119 GT 120
                                                                                                                                                              HV46_MOUSE
P01822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPOC
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DISULFID
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CONFLICT
CONFLICT
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                                                   Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 dvqlqesqpdlvkpsqslsltctvtgysitsgyswhwirqfpgnklewmgyihysgntsy 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIP$SHWWSWVPQPPARALEWIGEVFFSGSTIY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 gvnlresgpalvkathtltltctfsglsvntrgmsvswirgppgkalewlaridwdddky 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLLESGPGLVKPSGTLSLTGTVSGGSTPSSHWW-SWVPGPPGGKGLEWIGEVFFSGSIL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34, Indels 2, Caps
               MUS MUSCULUS (MOUSE).
BUKARYOTA; METAZOA: CHOPDATA: VEPTERPATA; TETPAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHOPDATA; VEPTEBPATA; TETPAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V-II REGION (SESS) V SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V PEGION (1843)
                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2
                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 419; DB 5; Length 147;
Pred. No. 1.57e-66;
26, Mismatches 34, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 431; DB 5; Length 116;
Pred. No. 3.41e-69;
18; Mismatches 21; Indels
                                                                                                                                         PROC. NATE. ACAD SCI U S A RI-5194-5198(1984)
PIR; A02090; GZHUCS.
HSSP; P01772; 1GGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 npslksrisitrdtsknqfflqlnsvttedtatyycar 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                     13158 MW; 10E4EE67 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (FEL. 05, CREATED)
13-AUG-1987 (FEL. 05, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V-II REGION (SESS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16323 MW; 0994FFF4 CPC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 AA
                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILAPITY
 IG HEAVY CHAIN PRECTIFICOP V PECTION (1843)
                                                                                                                                                                                                                                                                                                                                                                 FPAMEWORK 3
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TAKAHASHI N , NOMA T , HONJO T ;
                                                                                                                                                                                                                                       IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.6%;
Best Local Similarity 60.2%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.3%;
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hes 60, Conservative
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133
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147 AA;
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                                                                                         SEQUENCE FROM N A
                                                                                                         STRAIN-BALB/CJ;
MEDLINE; 89279149.
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68
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116
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1 EVOLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECUSOR V REGION (MOPC 141)
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
MUS MUSCULUS (MOUSE).
MUS MUSCULUS (MOUSE).
EUTHERIA: TETRAPODA; MAMMALIA:
EUTHERIA: RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V REGION (733).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 408; DB 5; Length 117;
Pred. No. 4.25e-64;
22, Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                     LEVY N S, MALTPIERO U V., LEBECQUE S.G., GEARHART P.J., J. EXP. MED. 169:2007-2019(1989).
PIR, JT0510; HVMS73.
HSSP; P01825; IBAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 ynpspksrttitrdtskngfflemnsltaedtatyycar 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YNPSLNDRVFMSVDRSKDQVSLRLSSVTAADTAVYYCAR 98
                                                       79 npslknrvsitrdtsenqfflklnsvttedtatyyca 115
                                                                                                                                                                                                                                                                                                                                                                                                    40 115 BY SIMILARITY.
117 117
117 AA; 13223 MW, 47664D8E CRC32;
                                                                                                                                                           01-NOV1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
10-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V REGION (773)
                                                                             61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 144 AA.
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EMBL, V00768; G51616; -.
PFIF; AC2004; G29874
HSSP, P01772; 1FDL.
IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN V REGION; SIGNAL.
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Best Local Similarity 56.6%;
Matches 56; Conservative
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117
115
117
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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 MEDLINE; 89279149.
                                                                                                                                                                                                                                                                                    STRAIN-BALB/CJ
                                                                                                                                      HV62_MOUSE
P18533;
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61 NPSLNDRVF-MSVDRSKDQVSLRLSSVTAADTAVYXCARSPIKMNGRM-MLDAFDIWGGG 119
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MEDLINE; 84024551.
MEDLINE; 84024551.
BIOCHEMISTRY 22.4291.4296(1983).
-!- THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE MONOCLONAL ANTIBODY
-!- THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE MONOCLONAL ANTIBODY
OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND IDLOTYPE FAMILY
CHAPACTERISTIC OF THE ANTIAPSONATE PESPONSE OF STRAIN A/J MICE.
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                                                                                                                                                                                                                                                                                                               1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (PRI. 01, LAST ANNOTATION UPDATE)
IG HEAYY CHAIN V REJION (36-60).
IG HEAYY CHAIN V REJION (36-60).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAZOA; CHORDATA: VERTERRATA: TETRAPODA: MAMMALIA:
                                                                                        Score 407. DR 5: Length 144;
Pred. No 7 07e-64;
26; Mismatches 30; Indeis
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19; Mismatches 20; Indels
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MEDLINE: 82059449.
OLLO R., AUFFRAY C., SIKOPAV J. -I., ROUGEON F.;
NUCLEC ACIDS RES. 94099-4109(1981).
EMBL: V00774; G51651; -.
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HSSP, P01825; 1HFM.
IMMUNGGLOBULIN V PEGTON; ANTIAPSONATE ANTIRONY.
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144 AA; 15759 MW; 10E3A531 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 npslksrisitrdtskngyylqlnsvtsedtatyyct 96
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21-JUL-1986 (REL. 01, LAST SEQUENCE HPDATE)
10-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PPECHESOR V REGION (441).
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Best Local Similarity 58.8%;
Matches 57; Conservative
                                                                                                        Query Match
Best Local Similarity 53.5%;
Matches 68; Conservative
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EUTHERIA; RODENTIA.
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HV47_MOUSE
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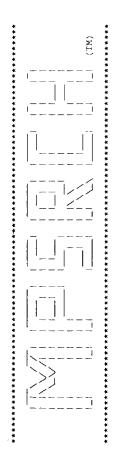
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                                                                                                                                                                                                                                                                                               1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTI- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 evkllesggglvqpggslklscaasgfdf-srywmswvrqapgkglewigeinpdsstin 59
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                                                                                                                                                                                                             Gaps
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PROC. NATL. ACAD. STI "S A 76.2890-2894(1979)
-!- THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN THAT BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 79223895
RAO D N., RUDIKOFF S., KRUTZSCH H., POTTER M.:
PROC. NATL. ACAD. SCI. U.S.A. 76.2894 (1979).
-!- THIS CHAIN WAS ISOLATED FPOM AN IGA MYELOMA PROTEIN THAT RINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKAPYOTA: METAZOA: CHOPDATA; VERTERPATA; TETPAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA, METAZOA, GHORDATA, VERTEBRATA, TETRAFODA, MAMMALIA.
EUTHERIA, RODENTIA.
                                                                                   IG HEAVY CHAIN V REGION (441).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 396; DR 5; Length 119;
Pred. No. 1 88e-61;
20; Mismatches 21; Indels
                                                                                                                                                                   DR 5; Length 116
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                             20, Mismatches 21,
                                                                                                                                                                                                                                                                                                                                      78 ytpslkdkfiisrdnakntlylgmskvrsedtalyycar 116
                                                                                                                                                                 Score 396; DR 5; 1
Pred. No. 1.88e-61;
                                                                                                                                                                                                                                                                                                                                                                              60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 ytpslkdkfiisrdnakntlylqmskvrsedtalyycar 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 YNPSLNDRVFMSVDKSKDQVSLPLSSVTAADTAVYYCAP 98
                                                             1 18 IS HEAVY CHAIN V
116 116
116 AA; 12911 MW; 44252075 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AA; 13169 MW; EEE850E1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE IPDATE)
21-JUL-1986 (PEL. 01, LAST ANNOTATION UPDATE)
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
HAVY CHAIN V REGION (X44).
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AA
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                                         IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 56.6%;
Matches 56; Conservative
                                                                                                                                                                     42.88;
                                                                                                                                                                                         Local Similarity 56.6%;
nes 56, Conservative
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HSSP; P01810; 1FVW.
IMMUNOGLOBULIN V PEGION.
PIR; A02076; HVMS44.
HSSP; P01810; 1FVW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 79223895
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P01807;
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P01808;
                                                                                                     NON_TER
SEQUENCE
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DR KET LES
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                                                                                                                                                                                                      1 EVQLLESGPGLVKPSGILSLICIVSGGSIRSSHWWSWVKQPPGKGLEWIGEVFFSGSII- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.7%; Score 395; DB 5; Length 119;
Best Local Similarity 55 6%; Pred. No. 3.13e-61;
Matches 55; Conservative 21; Mismatches 21; Indels 2; Gaps
                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BHAT TIN , NAVIA M A , COHEN G H , PAG DIN , PUDIKOFF
                                                                                                                                                                                                                                                                                                                                                                                                                           MOS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHOPDATA; VERTEBRATA: TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEINS 1:74-RO(1986)
--- THIS CHAIN WAS ISOLATED FPOW A MYELOWA PROTEIN THAI BINDS
                                                                                                        Score 396; DB 5; Length 119; Pred. No. 1 88e-61; 20; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 79223895.
PAO D.N., PUDIKOFF S., KRUTZSCH H., POTTER M.;
PROC. NATL. ACAD. SCI. U.S. A. 76·2890-2894(1979).
                                                                                                                                                                                                                                                        60 ytpslkdkfiisrdnakntlylqmskvrsedtalyycar 98
                                                             NON_TER 119 119 119 SEQUENCE 119 AA; 13246 MW; AICEB710 CRC32;
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13240 MW: 6892320D CEC32;
                                                                                                                                                                                                                                                                                                                                                                               , LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE)
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PDB; 2FBJ; 15-0CT-90.
IMMUNOGLOBULIN V PECION; 30-STPUCTUPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-PAY CPYSTALLOGPAPHY (2 A ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (PRL. 01, LAST SEQU
01-MAR-1992 (PRL. 21, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V PEGION (J539)
                                                                                                         Query Match
Best Local Similarity 56.6%;
Matches 56; Conservative
GALACTAN.
PIR; A02077; AVMSX4.
HSSP; P01810; 2FBJ.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 88217852.
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104
104
104
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                                                                                                                                                                                                                                                                                                                   LT 14
HV40_MOUSE
P01810;
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US-08-844-215-6.rsp

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1 evkllesggglvqpggslklscaasgfdf-sgywmswvrqapgkglewigeinpdsstin 59
                                                                                                                                                                                                                                                                                                                                                                 2; Caps
1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTI- 59
                                                                                                                                                                               HV41_MOUSE STANDARD; PRT; 117 AA.
P01811.
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
MUS MUSCULG (MOUSE).
MUS MUSCULG (MOUSE).
EUTHERRY, RETAZOA, CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.0%; Pred. No. 2.97e-59;
Matches 54; Conservative 23; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                60 ytpflkdkfiisrdnakntlflqmskvrsedtalyfcarn 99
                                                                                                                                                                                                                                                                                                                                                                                                           60 ytpslkdkfiisrdnaknslylqmskvrsedtalyycar 98
                                Search completed: Tue Feb 24 07:13:38 1998 Job time : 16 secs.
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Page 1



Pelease 2.10 John F. Collins, Riccomputing Pescarch Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Peb 24 07-41-10 1999, MasPar time 3.35 Seconds 191.725 Million cell updates/sec Pun on:

Tabular output not generated.

>US-08-844-215-6 (1-126) from US08844215.pep 925 I EVQLLESGPGLVKPSGTLSL Description: Perfect Score: Sedneuce.

PMMLDAFDIWGQGTLVIVSS 126

PAM 150 Gap 11 Scoring table:

56402 seqs, 5095871 residues Minimum Match 0% Listing first 45 summaries Post-processing: Searched:

Database:

a-issued libackl 2-51 3-52 4-53 5-54 4 55 7-55 8 PGT90 9.PGT91 l0 PGT92 ll:PGT93 12 PGT94 12 PGT91 14 PGT96

Mean 28.331; Variance 154.255; scale 0.184 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ			SUMMARIES		
Result No.	Score	Query Match	Query Match Length D	DB	ID	Description	Pred. No.
1	559	60.4	86	7	US-08-478-	Sequence 75, Applicati	1.31e-33
2	553	59.8	126	13	PCT-US95-0	142,	3.78e-33
m	553	59.8	126	7	38-27	C 3	3.78e-33
4	533	57.6	125	۲-	-80	76, A	1.28e-31
S	520	56.2	121	7	13.08.478	80,	Η.
9	509	55.0	139	۲	US-08-478-		8.66e-
7	506	54.7	121	۲-	.52-08-512	13,	
ω	502	54.3	120	Ć,	80	0)	2.96e-
6	502	54.3	120	11	PCT-US93-0	28,	2.96e-
10	502	54.3	120	۲.	US-08-211-	α,	C 1
11	200	54.1	110	Ľ	1-268û-IJd	Sequence 16, Applicati	4
12	478	51.7	124	7	US-08-478-	78,	
13	473	51.1	119	7	US-08-478-		4
14	471	50.9	134	۲-	-894-80-80	u)	ď
15	471	50.9	134	œ.	- 115-08-25d-	ď.	6.740-27
16	470	50.8	116	~	US-08-478-	Sequence 79, Applicati	
17	464	50.2	119	13	PCT-US95-1	62	2.29e-2
18	462	49.9	107	^	US-07-942-	C	3 250-2
19	459	49.6	119	1	-13-08-467-	62	5.486-
20	459	49.6	119	۲-	US-08-410-	9	5.486-2
21		48.1	129	Ξ,	1-8635-153	L'-	
C.	437	5.5	₹3° 1°4 1°4	۲-	US-08-211-	23	2 540-24

Page 2

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60 LESEVTMSRDISKNOFSVKLISVTAADIALYYCARENTGRITEEIG-NFFDIWGGGTLVI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                             US-08-276-852-142
                                                                                                                                                                                                                                                                                                                                                                         92037
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                                                 119 VSS 121
                                                                     124 VSS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIYNPS 63
                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSETLSLTCAVSGGSISSSYYWSWIRQPPGKGLEWIGYIYYSGSTYY 60
                                                                                                                                                                                                                                                       1 EVOLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 553; DB 13; Length 126;
Pred. No. 3.78e-33;
14; Mismatches 25, Indels 2, Caps
                                                                                                                                                                                                                     O, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                Score 559; DB 7; Length 98; Pred. No. 1.31e-33;
                                                                                                                                                                                                                    10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                126 AA.
                                                                                                                                                                                                                                                                                  61 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 98
                                                                                                                                                                                                                                                                                                      61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAR 98
                       012712-160
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 142:
                                                                                                                                                ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH4 consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 142, Application PC/TUS9508743
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 142, Application PC/TUS9508743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE. protein
JENCE 126 AA, 13684 MW, 88548 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                               98 AA; 10732 MW; 59041 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
NAME: TESKÍN ESG., RODÍN L. REGISTRATION NUMEER: 35,030 REFERENCE/DOCKET NUMBER: 012 TELECOMMUNICATION INFORMATION: 703-836-6620
                                                                                                        SS: not relevant
not relevant
                                                               INFORMATION FOR SEQ ID NO: 75: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 126 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                     LENGIH: 98 amino acids
                                     TELEPHONE: 703-000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                              peptide
                                                                                                                                                                                              Query Match
Best Local Similarity 78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7.

**Record 82; Conservative 82; Conservative 65.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                       SOURCE:
                                                                                                          STRANDEDNESS:
                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                PCT-US95-08743-142
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                                                                                                                                        ORIGINAL
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64 INDRVEMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNGGRMALDAFDIWGGGLIVI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lerner, Richard A VENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIHODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS: 18
ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No 562138th Torrey Fines Road, Suite 220, STREET: 10666 No 7672138th Torrey Fines Road, Suite 220, STREET: 10666 No 772138th Torrey Fines Road, Suite 220, STREET: 10666 No 772138th Torrey Fines Road, Suite 220, STREET: 10666 No 772138th Torrey Fines Road, Suite 220, STREET: 10666 No 772138th Torrey Fines Road, Suite 220, STREET: 10666 No 772138th Torrey Fines Road, Suite 220, STREET: 10666 No 772138th Torrey Fines Road, Suite 220, STREET: 10666 No 772138th Torrey Fines Road, Suite 220, STREET: 10666 No 772138th Torrey Fines Road, Suite 220, STREET: 10666 No 772138th Torrey Fines Road, STREET: 10666 No 772138th Torrey Fines Roa
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Local Similarity 66 7%: Prod No 3 78e-33;
Local Similarity 66 7%: Prod No 3 78e-33;
Local Similarity 65 7%: Prod No 3 78e-33;
Local Similarity 65 7%: Prod No 3 78e-33;
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                         126 AA.
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FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
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APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954.148
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SYSTEM: PC-DOS/MS-DOS
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JENGE 125 AA; 13684 MW; 88548 CN;
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Patent No. 5652138
GENEPAL INFORMATION:
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TELECOMMINICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 142:
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Carlos F
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Barbas,
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4 LLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIYNPS 63
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APPLICANT: Hanna, Nabil
APPLICANT: Radb, Ronald W
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CORRESPONDENCE ADDRESS:
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CITY: Alexandria
STATE: VA
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FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Teskin Esq., Robin L
REGISTRATION NUMBER: 35.030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
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COMPUTER: IRM PC COMPATIBLA
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 76, Application US/08478039 Patent No. 5681722 GENERAL INFORMATION:
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INFORMATION FOR SEC 1D NO: 76-
SEQUENCE CHARACTERISTICS:
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                                                                                                                                       119 VSS 121
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61 YNPSLKNRVIISVDISNNQFSLKMISVIAADTAIYYCARGDVI-S-GWYR-GYFDSWGQG 117
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                                                                                                                                                                                    1 QMQLQESGPGLVKPSETLSLTCAVSGGSISSSYDWTWIRQPPGMGLEWIAVISGNSGSAD 60
                                                                                                                                                                                                                                        1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVF-FSGSTI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Hannan Therapy
NUMBER OF SEQUENCES: 114
                                                COMPUTER PEADABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERALING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TELEPOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
VH4 clone 4-14
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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25-JAN-1995
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                      125 AA; 13363 MW; 90929 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80, Application US/08478039 Patent No. 5681722 GENEPAL INFORMATION:
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REGISTRATION NUMBER: 35,03(
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APPLICATION NUMBER: US 08/
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
FILING DATE: 10-JUL-1992
FILING DATE: 10-JUL-1992
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                          / Match
Local Similarity 63.0%;
les 80; Conservative
CHROMOSOME/SEGMENT:
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CITY: Alexandria
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ZIP: 22313-1404
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                      SEQUENCE
                                                                             Query Match
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RESULT
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                                                                                                                                                                                        1 QVQLQEAGPGLVKPSETLSLTCSVSGGSISGDYYWFWIRQPPGKGLEWIGYIYGSGGGTN 60
                                                                                                                                                       7; Gaps
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TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCE: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 PRINGE St.
CITY: Alexandria
                                                                                                         Score 520, DB 7; Length 121;
Pred. No. 1.25e-30:
19; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                 CHROMOSOME/SEGMENT: VH4 anti-CD4 CHIM NCE 121 AA; 13232 MW; 88649 CN;
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07-308-1995
N: 435
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APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
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APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 07/735,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          Sequence 108, Application US/08478039
                                                                                                                                                                                                                                                                                                                          Sequence 108, Application US/08478039.
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Newman, Roland A. APPLICANT: Hanna, Nabil APPLICANT: Raab, Ronald W.
                              STRANDEDNESS: not relevant TOPOLOGY not relevant
                                                                                                                                                                                                                                                                        STANDARD;
    SEQUENCE CHAPACTEPISTICS.
LENGTH: 121 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                 peptide
                                                                                                             Match
Local Similarity 63.0%;
les 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     Patent No. 5681722
GENERAL INFORMATION:
                                                                  ORGANISM: Monkey POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                       SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                               STRANDEDNESS:
                                              MOLECULE TYPE:
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                                                                                                                                                                                                                    115 VLVTVSS 121
                                                                                                                                                                                                                                     120 TLVIVSS 126
                                                            ORIGINAL
                                                                                                                                                                                                                                                                                                           01-JAN-1900
                                                                                             SEQUENCE
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                            XXXXXX
                                                                                                                                 Matches
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TITLE OF INVENTION: Recombinant human anti-human immunodeficiency TITLE OF INVENTION: virus antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 YNPSLNNRVSISIDISKNLFSLKLRSVTAADTAVYYCASNILKYLH-WL-L--Y--WGVG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 65.4%; Pred. No. 1.47c-29;
Matches 83; Conservative 12; Mismatches 25; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLQEAGPGLVKPSETLSLTCSVSGGSISGDYYWFWIRQSPGKGLEWIGYIYGSGGGTN 79
                                                                                                                                                                                                                                                                                                                                                                                                          7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,053
                                                                                                                                                                                                                                                                                                          Length 139;
                                                                                                                                                                                                                                                                                                                                                20; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AA.
                                                                                                                                                                                                                                                                                                            55.0%; Score 509; DB 7; 1
61.9%; Pred. No. 8.66e-30;
                                     ALLENAL PASKIN ESG., Robin L.
REGISTRATION NUMBER: 75,030
REGISTRATION NUMBER: 012712-160
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 336-6620
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy DC-DOS/MS-DOS
                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 139 AA: 15445 MW: 115855 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE 121 AA; 13365 MW: 86912 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/08275053
Patent No. 5607847
GENEPAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08275053.
                                                                                                                                            TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 121 amino acids
amino acid
FILING DATE: 25-JUL-1991
ATTOENEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCI
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    : 139 amino acids
amino acid
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
                                                                                                          LECUMAN: 703-62-2021
                                                                                                                                                                                                                                                                                                                                   Dest Local Similarity 61.9%;
Matches 78, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-275-053-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TLVIVS 125
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                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                       Query Match
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6.0 YNPSLNIPVEMSVDKSKFQVSLPLSSVIAADTAVYYARSPIKMNGSRMH.DAFDIMGGG 119 61 YSPSIKSFVIMLFDISKNUÐSLFLSSVIAAFHAVYYGAFB----NHG-II-ISMDYMGOG 114

115 SLVTVS 120

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1 EVQLLESGPGLVKPSGILSLICIVSGGSIRSSHW-WSWVRQPPGKGLEWIGEVEFSGSTI 59

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60 YNPSLNDPVEMSVDKSKPAVSLPLSSVTAADTAVYYCAPSPIKMNGGRMMLDAFDIWGOG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 502; DB 6; Length 120;
Pred. No. 2.96e-29;
12: Mismatches 25; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Rorun
STREET: 6300 Sours Tower, 233 5 Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE. Patentin Palease #1.0, Version #1 25 CURRENT APPLICATION DATA
                                                                                                                      120 AA
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HIV Immunotherapeutics NUMBER OF SEQUENCES: 38 COPPESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT/US92/07111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA-
APPLICATION NUMBER- 32 07/748,562
FILING DATE: 22-NG-1991
PRIOR APPLICATION DATA-
APPLICATION NUMBER- PCT/US92/07111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/039,457 FILING DATE: 22-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PECISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 120 AA; 13278 MW; 84976 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/111,080
                                                                                                                                                                                                                  Sequence 28, Application 08/111080
                                                                                                                                                                                             Sequence 28, Application 08/111080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELET: 25-3856
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 amino acids
                                                                                                                      STANDAPD
                                                                                                                                                                                                                            Patent No. 5558865
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borun, Michael F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match
Local Similarity 65.1%;
nes 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER PEADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER.
                                                                                                                                                                                                                                                                                                                                            COUNTRY: Infinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
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                                                                                                                     US-08-111-080-28
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120 TLVIVSS 126
                                               115 SLVTVSS 121
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TOPOLOGY:
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                                                                                                           RESULT
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1 QVQLQESGPGLVRPSQTLSLTGTVSGFSTTSSSYCWHWVPQPPGPGLEWIGPICYEGSID 60

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVRPSQTLSLTCTVSGFSITSSSYCWHWVRQPPGRGLEWIGRICYEGSID 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHW-WSWVPQPPGKGLEWIGEVFFSGSTI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 502; DB 11; Length 120;
Fred. No. 2.95e-29,
12; Mismatches 25, Indels 7; Gaps
                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Falease #1 0, Version #1.25 CUPPENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
                                                                                                                                                                                                                                                           6300 Sears Tower, 233 S Wacker Drive
                                                  120 AA.
                                                                                                                                                    Sequence 28, Application PC/TUS9307967
GENERAL INFORMATION
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
COPPESSONDENCE ADDPESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PPIOR APPLICATION DATA:
APPLICATION NUMBER. PCI/US92/07111
FILING DATE. 24.AUG.1992
PPIOP PAPPLICATION DATA
APPLICATION NUMBER: US (08/039,457
                                                   PRT;
                                                                                                                             Sequence 28, Application PC/TUS9307967.
                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 120 AA; 13278 MW; 84976 CN;
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TORNEY/AGENT INFORMATION NAME: Borun, Michael F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEGISTRATION NUMBER: 25,447
PEFEDENCE/DOCKET NUMBER: 310
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (312) 474-53:00
TELEFAX. (322) 474-5448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 22-AFR-1993
ATTORNEY/AGENT INFORMATION:
                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 54.3%;
Local Similarity 65.1%,
les 82; Conscrvative
                                                                                                                                                                                                                                                                           COUNTRY: HEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                            STREET, 6300 S
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                  PCT-US93-07967-28
                                                                                                                                                                                                                                                                                                                90909
                                                                                                                                                                                                                                                   ADDPESSEE
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120 TLVIVS 125
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                                                                                                     01-JAN-1900
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                                                                               XXXXXX
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119 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FION: 1..119
119 AA; 13135 MW; 76375 CN;
                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                Sequence 16, Application PC/TUS9310555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                  APPLICANT: SILVERMAN, GREGG J. TIILE OF INVENTION. METHOD FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFOPMATION FOR SPQ ID NO: 16:
                                                                                                                                                                                                                                                                       TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1993
                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.1%;
Local Similarity 62.5%;
es 75; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER PEADABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                 Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                          TITLE OF INVENTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                            PCT-US93-10555+16
                                                                                                                                                                                                                                                                                                                                                                     90067
                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
       115 SLVTVS 120
                               120 TLVIVS 125
                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE:
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                                                                                                                              01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNGGRMMLDAFDIWGGG 119
1 QVQLQESGPGLVRPSQTLSLTCTVSGFSITSSSYCWHWVRQPPGRGLEWIGRICYEGSID 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVOLLESGPGLVKPSGTLSLTCTVSGGSIRSSHW-WSWVRQPPGKGLEWIGEVFFSGSTI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 502; DB 7; Length 120; Pred. No. 2.96e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches 25; indels
                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
                                                                                                                                                                                                                                                                                                               STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago
                                                                                                            120 AA.
                                                                                                                                                                                                                                                     TITLE OF INVENTION: HIV Immunotherapeutics NUMBER OF SEQUENCES: 38 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US92/07111
PILING DATE: 24 ANG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
BENCE 120 AA; 13278 MW: 84976 CN;
                                                                                                                                                                                                       Sequence 28, Application US/08211980
Patent No 5665569
                                                                                                                                                                                  Sequence 28, Application US/08211980.
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Borun, Michael F. REGISTRATION NUMBER: 25
                                                                                                               STANDARD
                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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Best Local Similarity 65.1%;
Matches 82, Conservative
                                                                                                                                                                                                                                                                                                                                         Illinois
: USA
                                                                                                                                                                                                                                                                                                          Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   90909
                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                               US-08-211-980-28
                                       115 SLVTVS 120
                                                              120 TLVIVS 125
                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                              01-JAN-1900
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                                                                                                                                        XXXXXX
                                                                                                      RESULT
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TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY PESTPICTED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 NPSLISRVIMSLDISKNQFSLKLISVIAADIAVYYCARGPCEAYCTDDAPOAYFCHWGOG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNQGRMMLDA-FTITWGQG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLQQWGAGLLKFSETLSLTCAVYGGPF-SGYYWSWVPQPPGKGPFWIGEINHSGRTTY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Mismatches 27; Indels 2: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 500; DB 11; Length 119;
Pred. No. 4 20e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                     E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
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1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSS-HWWSWVRQPPGKGLEWIGEVFFSG-ST 58

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TITLE OF INVENTION: Recombinant Antibodies for Human Therapy NUMBER OF SEQUENCES: 114 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 478; DB 7; Length 124;
Pred. No. 1.98e-27;
14; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/412,242
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/412,242
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/7856,281
APPLICATION NUMBER: US 07/7856,281
                                                                                                                                                                                             STREET: BURNS, POANE, SWECKER & MATHIS STREET: 699 Prince St.
CITY: Alexandria
               124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     012712-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VH4 clone 4-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07.7735 OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/735.064
FILING DATE: 25-40L-1991
ATTORNEY/AGENT INFORMATION:
              PFT;
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AA; 13147 MW; 95091 CN;
                                                                                                             Sequence 78, Application US/08478039
Patent No 5681722
                                                                                      Sequence 78, Application US/08478039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET UNBER: 012
TELECOMMUNICATION INFORMATION.
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS: not relevant not relevant
                                                                                                                                                 APPLICANT: Newman, Roland A. APPLICANT: Hanna, Nabil APPLICANT: Raab, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 amino acids
               STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22313-1404
COMPUTER READARIE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.7%;
Best Local Similarity 62.5%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                         Patent No 5681722
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
             US-08-478-039-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IOPOLOGY:
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                                                              01-JAN-1900
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                                        XXXXXX
RESULT
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1 QVHLQESGPGLVKPSETLSLTGSVSGSISSSGYYWGWIPQPPGKGLEWIGSIHGSGGSN 50

7; Gaps

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61 SLNPSLKSRVTLSVDTSGNKFSLKLSSVTAADTAVYFCARE---LYSSSPYY--FDFWGO 115
                                                                                                                                                                                                                                                             APPLICANT: Newman, Roland A. APPLICANT: Hanna, Nabil AFFLICANT: Hanna, Nabil AFFLICANT: Raab, Ponald W. TITLE OF INVENTION: Percombinant Antibodies for Human Therapy COPPRESPONDENCE: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                 WEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-001-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: Z6-181-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: Z6-181-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
APPLICATION NUMBER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                               ADDPESSEE: RUPNS, FOANE, SWECKER & MATHIS STREET: 699 Prince St. CITY: Alexandria
                                                                                                                              119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFFLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,030
REFERENCE/POCKET NUMBER: 012712-160
                                                                                                                              PPT;
                                                                                                                                                                                                                              Sequence 77, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
                                                                                                                                                                                                        Sequence 77, Application US/08478039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN ESG., ROBIN L.
PEGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
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                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER PEADABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPSANISM: Monkey
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIF: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POSITION IN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                    116 GVRVTVSS 123
                                                                           119 GTLVIVSS 126
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                                                                                                                            US-08-478-039-77
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8888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRODUCTION OF HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR HEPATITIS B SUPFACE ANTIBODIES
                                                                                                                                             1 QVQLOESGPGLVKPSETLSLTCAVSGGSISSGYYWGWIRQTPGKGLEWIGSLOGPGGNKY 60
                                                                                                                                                                                  1 EVOLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                                                Length 119;
                                                                Query Match
Best Local Similarity 68.7%; Pred. No. 4.75e-27;
Matches 68; Conservative 11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

RELIAND DATE: 05-711N. 10-711N. 10-711N. 10-71N. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                   61 INLCLKSRVTLSADTSKNOFSLKLSSVTAADTAVYYCAR 99
                                                                                                                                                                                                                                                         NAME: Smith, William M. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 11823-50-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 06/904,517
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15-JUN-1990
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           VH4 clone 4-14
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                 CHROMOSOME/SEGMENT: VH4 clone 4
ace 119 AA; 12636 MW; 81453 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08468671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08468671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WERAL INFORMATION:
APPLICANT: OSLDEIG, LAIS G.
TITLE OF INVENTION: PRODUCT
TITLE OF INVENTION: ANTIBOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 15-JUN-1
RIOR APPLICATION DATA:
APPLICATION NUMBER I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5648077
                                                                                                                                                                                                                                                                                                                                                    T 14
US-08-468-671-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXXX
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ANTIBODIES SPECIFIC FOR BEPATITIS B SURFACE ANTIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QVOLOESGPGLVKAAETLSLTCTVSRGSF-SDYFWNWFRQPAGKRLEWLGRVYTSGSVDY 78
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCHONAL
TITLE OF INVENTION: ANTIHODIES SPECIFIC FOR HEPATIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC.LOS/MS-LOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 NPSLKSRVIVSVDISKKQFSLRLSSVIVADIAVYYCARG 117
                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 69.7%; Pred. No. 6.74e-27;
Matches 69; Conservative 11; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-1994
14-JUN-1994
1N: 424
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APPLICATION NUMBER: US 07/192,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    us ok/425,196
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PRIOR APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07/538,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE, protein
JENCE 134 AA; 14995 MW; 109187 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08259372A
Patent No. 5565354
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08259372A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0K/0
FILING DATE: 31-0CT 1986
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 21-APP-1942
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US U7/Y
FILING DATE 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/Y
TELECOMMUNICATION INFORMATION:
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                         TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                       134 amino acids
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94111-3834
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                                                                                                                                                                                                                                                                                       linear
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US-08-259-372A-6
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                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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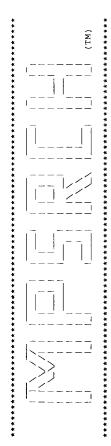
```
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERFICTICS:
LENGTH: 134 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 134 AA: 14995 MW: 109187 CN;
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Score 471, DB 6, Length 134, Pred. No. 6.74e-27; 11; Mismatches 18; Indels 1; Gaps 1; Query Match 50.9%, Best Local Similarity 69.7%; Matches 69; Conservative

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79 NPSLKSRVTVSVDTSKKQFSLRLSSVTVADTAVYYCARG 117 aa

Search completed: Tue Feb 24 07:41:23 1998 Job time : 13 secs.



Release 2.1D John F. Collins, Biccomputing Pescarch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Fob 24 07:14:35 1998; MasPar timo 6.79 Seconds 257.613 Million cell updates/sec Run on.

Fabular output not generated.

.. PMMLDAFDIWGQGTLVIVSS 126 >US-08-844-215-6 (1-125) from US09844215.pep 925 1 EVOLLESGPGLVKPSGTLSL. Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

111726 seqs, 13889129 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseg30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9.part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part15 13:part21 20:part12 23:part13

Mean 30.712; Variance 168.307; scale 0.182 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		0					
Pesult No.	Score	Query Match	Query Match Length	DB	ID	Description	Pred. No.
. et	618	66.8	124	20	W06474	Human lung cancer spe	5.59e-37
CI	583	63.0	142	7	R41285		2.54e-34
m	267	61.3	117	12	R66320	Human immunoglobulin	4.15e-33
4	267	61.3	117	ω	R40953	Human germ-line gene	4.15e-33
2	559	60.4	124	C.	R12266	Anti-human RhD PAG-1	1.580-32
9	558	60.3	127	cı	P12265	Anti-human PhD Pod-R	1 990-32
7	558	60.3	475	19	इन्द्रम	Monoclonal antibody D	1 990-32
80	556	60.1	9.00	C.	F12269		2.926.2
σ	553	59.8	126	0	P54270	Anti-HIV gp41 immuneq	4 776-32
10	553		126	9	W01315	ab DL 4	4.77e-32
11	550	59.5	116	7	R42689	vh 71-4.	
C.	550		116	(4	R66346	Human immunoqlobulin	8.04e-32
13	550	59.5	476	0	W01822	Primatised anti-human	8.04e-32
14	549	σ'n	118	12	R66348	Human immunoglobulin	9.57e-32
15	548		136	C4	W24536	Immusoglobulin rB6B7	1.136.31
16	547	6	118	13	R55329	Human immunoqlobulin	1.36e-31
	547	6	122	ų,	P30145	MAD 1-3-1 variable re	1 360-31
18	545	58.9	116	4	F66298	Human immunoglobulin	1.920.21
19	3	58.2	138	U)	P29014	pric-RVh-PM1f-4	6.500-31
20	538	58.2	138	u)	F29032	PTC-PVh-PM1f	6.50e-31

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73e-3 20e-3 20e-3 10e-3	246-3 236-3 416-3 506-2	CONTRACTOR OF CO		)
Tebuli monoc recom glucu	man immunoglobulin manised anti-CEA s 26 1/26 VH hum riable region of h	4 0 0 0 6	PER	בליינים ביינים ביינים
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# ALIGNMENTS

SOURCE SEED AND WASHELL TETTETTETTETTETTETTETTETTETTETTETTETTET	W06474 standard; Protein; 124 AA. W06474 standard; Protein; 123-MAY-1997 (first entry) Human lung cancer specific antibody heavy chain variable region; human; monoclonal antibody; lung cancer tissue; diagnosis; purification; cancer-specific antigen; ss. Homo saplens. Location/Qualifiers Region /label= CDR1 /label= CDR2 /label= CDR2 /label= CDR3 /label= CDR
Quc Bes Mat	Query Match 66.8%; Score 618; DB 20; Length 124; Best Local Similarity 71.4%; Pred. No. 5.59e-37; Matches 90: Conservative 13: Mismatches 21, Indels 2. Gaps 1;
Jan.	30) COMBETVALLY TO MISMACCIES ET LINCES ET GAPS

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F105 rearranged variable region heavy chain.
Monoclonal antibody: MAb; envelope; glycoprotein; gp120; HIV; AIDS;
CD4; receptor, hybridoma; polymerase chain reaction, FCR, heavy, light;
                                     61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNQGRMMLDAFDIWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monitoring HIV infection
Claim 9-10; Page 77: 109pp; English.

Claim 9-10; Page 77: 109pp; English.

MRNA from the known hybridona Fl05 was converted to CDNA and this subjected to PCK amplification using primers corresp. to appropriate parts of the heavy or light chains and having restriction sites to permit cloning. The extension prods. Were isolated and sequenced. The recombinant human monoclonal antibody (MAb) binds to a discontinuous epitope on the HIV gpl20 envelope glycoprotein, blocks the binding of gpl20 to the CD4 receptor, and neutralises a broad deficiency, esp at doses of 0.1-10 mg/kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 spslksrvtisvetsknqfslkltsmtaadtavyycargpvpavfygdyrldp---wqqg 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 npslksrvtisadtsknqfslkvnsvtaadtavyycarrnydfwsggd--gpfdywgggt 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1995 (first entry)
Human immunoglobulin variable heavy chain #26.
Primer: PCP: amplify: human: immunoglobulin; variable; heavy chain: cosmid; placenta: vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA segments encoding monoclonal antibody - which binds to {\tt gpl20} and neutralises HIV, for treating ALDS, and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 583; DB 7; Length 142; Pred No 2 54e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marasco WA, Posner MR, Sodroski JG;
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(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                 chain; epitope; immune deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R66320 standard; Protein; 117 AA.
                                                                                                                                                                                    R41285 standard, Protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.0%;
Best Local Similarity 68.5%;
Matches 87; Conservative
                                                                                                                                                                                                                     01-NOV-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         20..142
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1992; U10928.
10-DEC-1991; US-804652.
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                                                                                                                                                                                                                                                                                                                                                                          /label= sig_peptide
Protein 20..
                                                                                                                                                                                                                                                                                                                                                                                                           /label- mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deficiency, esp a'
Sequence 142 AA;
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WPI; 93-214174/26.
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                                                                        119 lvtvss 124
                                                                                                           121 LVIVSS 126
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                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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WO9426895-A.
                                                                                                                                                                                                                                                                                                                                                      Peptide
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production of human immunoglobulin in mammalian hosts
Disclosure, Page 67-68; 130pp; Japanese.
Disclosure, Page 67-68; 130pp; Japanese.
Prictin sequences (P66295-51) are nevel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (178949-79602) were isolated and cloued from a series of cosmid constructs: Y202: Y103: Y21: Y6;Y24: 3-31; M84; M18 and M131, by PGR umplification using primers (78917-38. The genes are subdivided into 5 families of VH genes. The fragments cover a region of Ren kh Phe INA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with Tag restriction enzyme. The Fragments were separated by gel electophoresis and 35-45 kb fractions were collected. The fragments were ilgated with Clal-digested cosmid vector pJ881. The flightion
                                                                                                                                                                                                                                                                                                                                                                      The Vh genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 gyglgesgpglykpsdtlsltcavsgysisssnwwqwirgppgkglewiqyiyysqs*yy 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1994 (first entry)
Human germ-line gene DP-68/JH6 antibody heavy chain.
humanised antibody: human germ-line; heavy chain; variable region;
framework region, teshaped antibody. CDE grafted antibody;
complementarity determining region; immuno silent.
                                                                                                                          DNA fragment comprising human immunoglobulin Vh genes - for the
                                                                                                                                                                                                                                                                                                                                                fragments were in vitro packed and infected into E.coli 490A. fragments were then subcloned by colony hybridisation. The Vh the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 567; DR 12; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.15e-33;
11; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R40953 standard; protein; 117 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.6%;
Matches 76; Conservative
                                                  (NISB) JAPAN TOBACCO INC.
Honjo I, Matsuda F;
WPI; 95-006791/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= FR1
/note= "framework region"
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19-FEB-1992; GB-003459.
(SCOT-) SCOTGEN LTD.
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                                   WO-JONEOS.
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24-NOV-1994.
10-MAY-1993; J00603.
10-MAY-1943; WD-,TODK
                                                                                                      N-PSPR: 078966
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RESULT
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Disclosure: Fig 5, 32pp; English.

The DNA sequence of eleven monoclonal antibodies are represented in 0119145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols, having varied binding specificity. The chimaeric anti-RhD antibodies can be used for diagnosis and therapy, and are capable of providing bloodbe used in passive immunisation to prevent haemolytic disease of the
                                                                                                                                                                                                                                                                                                                                                                              1 qvqlqesgpglvkpsdtlsltcavsgysisssnwwgwirqppgkglewigyiyysgstyy 60
                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLLESGPGLVKPSGTLSLITTVSGGSIPSSHWWSWVPQPPPRKALEWIGFVFFSGSTIY 60
                                                                     A humanised antibody comprised CDPs cirginally from a mouse MAD RSV19 specific for Respiratory Syncytial Virus transplanted onto heavy and light chain V region domains derived from NEWA and REI myeloma proteins, respecively. The framework regions of this CDP-grafted antibody were converted to the germ-line equivalent For conversion of the H-chain, the germ-line heavy chain DP6B/JH6 (R40953) was used, Germ-line framework regions are those present in Immature B cells, i.e. prior to any somatic mutation which takes place during maturation. Unlike mutations in the CDRs, any mutation
                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                          in framework regions does not affect affinity for an antigen and is therefore essentially random. The mutation may, however, cause the "self" antibody to be recognised as "foreign" and conversion to the unmutated germ-line sequence renders the framework regions "immuno
            New altered antibodies with reduced immune responses - have germ-line aminoacid residues replacing somatically mutated
                                                                                                                                                                                                                                                                                                                  Score 567, DB 8, Length 117, Pred. No. 4.15e-33; 11; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-AUG-1991 (first entry)
Anti-human RhD PAG-1 MAP (VH rhain)
Monoclonal antibody; rhesus D; blood-typing; CDR;
haemolytic disease of the newborn; HDN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NPSLNDRVFMSVDKSKRROVSLPISSVTAADTAVYYGAP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 npslksrvtmsvdtsknqfslklssvtavdtavyycar 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                         Example 3; Fig 4a; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P12266 standard: Protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-1989; GB-025590.
(BLOO-) CENT BLOOD LAB AUTH.
                                                                                                                                                                                                                                                                                                                  Ouery Match 61.3%.
Best Local Similarity 77.6%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31..35
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                                                                                                                                                                                                                                                                                       117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hughes- Jones N;
WPI; 91-178104/24
WPI; 93-288411/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- CDR3
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                                                                                                                                                                                                                                                                                       Sequence
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                                           residues
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Score 559; DB 2; Length 124;

60.48;

Query Match

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The DNA sequence of eleven monoclonal antibodies are represented in 011945-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols, having varied binding specificity. The chimaeric anti-khi antibodies can be used for diagnosis and therapy, and are capable of providing bloodtyping reagents of high specificity and reliability. They can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 npslrsrvtisvdtskngfslklgsvtaadtavyycarvlysrtisgysy-ymdywgkgt 118
                                                                                                                                                                                                                                                           61 NPSLNDPVFMSVDKSKDDVSLPLSSVTAADTAVYYCARSPIKMNQGRMMLDAFDIWGQGT 120
                                                                                     1 qvqlqesgpglvkpsetlsvtctvsggsvsssyw-swirqppgkgpewigyiyysgstny 59
                                                                                                                                         1 EVALLESGPGLVKPSGTLSLICIVSGGSLPSSHWWSWVPQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lypuny Leayents of nigh specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the members.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVALLESGPGLVKPSGILSLICIVSGGSIESS-HWWSWVRQPPGKGLEWIGEVFFSGSII 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 558; DB 2; Length 127;
Pred. No. 1.996-32;
18; Mismatches 27; Indels 1: Gaps
                           Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding complementary determining regions - of human
Best Local Similarity 65.9%; Pred. No. 1.68e-32;
Matches 83, Conservative 15; Mismatches 26, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-rhesus D antibodies, useful in prodn. of monoclonal antibodies and for passive immunisation Disclosure; Fig 4; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-human RhD FOG-B MAD (VH chain).
Mundelenal antibody, thesus D. blood-typing; CDR;
haemolytic disease of the newborn; HDN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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R12265 standard; Protein; 127 AA.
R12265;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-1989; GB-025590.
(RL70-) ZENT BLOCD LAP AUTH.
Hughes Jones N:
WPP: 91-178104/24.
N-PSDP: Q11947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62.8%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100..116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1990; E01964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AA;
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Matches
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The sequences given in R93553-54 represent the heavy and light chains respectively of a monoclonal antibody against a 65 kG antigen of human cytomegalovirus (hCMV). The DNA's encoding these sequences were amplified using the sequences given in T18040-58. The monoclonal antibody may be used in the diagnosis of hCMV.
                                                                                                                                                                                                                                                                                                                                                                                                       80 ynpslksrvtisvdasnnqfslklssvtaadtavyycartspqyyd--lltgsfpsywgq 137
                                                                                                                                                                                                                                                                                                                                                                                                                              60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNQGRMMLDAF-DIWGQ 118
                                                                                                                                                                                                                                                                                                                                                                            20 glglgesgpglvkpsetlsltctvsgdsisrssyswgcirgppgkglewigtiyysgsty 79
                                                                                                                                                                                                                                                                                                                                           Gaps
            20-AUG-1996 (first entry)
Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
Polymerase chain reactions primer, amplify; PCR: light chain; MAb;
65 kD antigen; human cytomegalovirus; hCMV; heavy chain: diagnosis.
                                                                                                                                                                                                    Human monoclonal antibody binds to cytomegalovirus 65 kD antigen
                                                                                                                                                                                                                 produced by primer amplification, used in the diagnosis of hCMV
                                                                                                                                                                                                                                                                                                                                            -7
                                                                                                                                                                                                                                                                                                                      Score 558; DB 16; Length 475, Pred. No. 1.99e-32; Indels 18; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding complementary determining regions · of human anti-rhesus D antibodies, useful in prodn. of monoclonai antibodies and for passive immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-1991 (first entry)
Anti-human RhD FOM-1 MAB (VH chain).
Monoclonal antibody; rhesus D; blood-typing; CDR; haemolytic disease of the newborn; HDN.
                                                                                                                                                                                                                                     laim 4; Page 16-18; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .T 8
R12269 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1990; E01964.
13-NOV-1989; GB-025590.
(BLOO-) CENT BLOOD LAB AUTH.
                                                                                                                                                                                                                                                                                                                        60.38;
                                                                                                          /note- "Mature heavy chain"
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 66.4%;
Matches 85; Conservative
                                                                                                                                                           (NISN ) NISSHINBO IND INC.
(TANA/) TANAKA H.
API; 96-154852/16.
                                                                                   "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31..35
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                                                                                                                                                    18-FEB-1994; JP-021628
                                                                                                                               13-FEB-1996.
20-FEB-1995; 030742.
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; 91-178104/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 gtlvtvss 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 GTLVIVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q11951
                                                                                                                                                                                             N-PSDB; T18059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9107492-A.
                                                                                                                   J08038178-A.
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                                                        Synthetic.
                                                                                                                                                                                                                               ntection
                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                Protein
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                                                                           Peptide
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The DNA sequence of eleven monoclonal antibodies are represented in 0119145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols, having varied binding specificity. The chimaeric anti-RHD antibodies can be used for diagnosis and therapy, and are capable of providing bloodtyping reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 212; 248pp: English.

Lymphocyte mRNA was converted to CDNA and subjected to PCR amplification using primers specific for heavy and light chain variable regions. The amplification products were inserted into a dicistronic vector to produce a library of fragments. E.coli XLI Blue cells were transformed with the library. Filamentous phage were produced which expressed the MAD regions on their surface. Panning with gpl20 and gp41 resulted in the recovery of immunoractive clones. The heavy chain VH region sequence R54270 neutralises HIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 qvqlqqwgagllkpsetlsltcavyggsf-sgyywnwirqppqkqlewiqeiihsqstny 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4) Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-HIV gp41 immunoglobulin heavy chain V region clone DL 41 19. Human immunodeficiency virus; HIVI; glycoprotein gp41; epitope; neutralisation; monoclonal antibody; heavy chain; variable region; framework region; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gp120 or gp41 and nucleic acid encoding them, useful for in vivo or in vitro diagnosis and for passive inmuno-therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human monoclonal antibodies neutralising HIV - react with
                                                                                                                                                                                                                                                                                                                            Length 128;
                                                                                                                                                                                                                                                                                                                                                                                   22; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                               Score 556, DB 2, Pred, No. 2.83e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R54270 standard; protein: 126 AA.
Disclosure; Fig 8; 32pp; English.
                                                                                                                                                                                                                                                                                                                               Match 60.1%;
Local Similarity 62.8%;
Local Similarity 62.8%;
Local Similarity 62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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(SCRI ) SCRIPPS RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burton DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47..62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 kgttvtvss 128
                                                                                                                                                                                                                                                                                 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 QGTLVIVSS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09407922-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barbas CF,
                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                         newborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R54270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Podion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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90 A

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/label= sig_peptide
Protein 20..
                                                                                                                                                                                                                                                                                                                                                                                                      'label= mat_protein
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                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                     'label≈ CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR2
                                                                                  119 vss 121
                                                                                                                    124 VSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 - JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                           vh 71-4.
                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R66346;
                                                                                                                                                                                                          P42689;
                                                                                                                                                                                                                                                                                                                                                                                                                          Reg 10n
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                       RESULT
                                                                                 QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       passive immunor therapy and detection of HIV infection.

Example 3: Fig 18: 366pp; English.

Example 3: Fig 18: 366pp; English.

Example 3: Fig 18: 366pp; English.

Free sequences given in W01315-19; represent the heavy chain variable regions (VH) of a series of antibody fragments (FAb's) which are immunoreactive with HIV glycoprotein gp41. This sequence represents chains which bind to the light chain clones given in W0130-24. A monoclonal antibody containing one of these Pab sequences may have the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/m1.

The MAD may be used for determining immunocompetence of a human anti-HIV antibody and in the detection of HIV infection.
                                                                                                                                                                       60 lrsrvtmsrdtskngfsvkltsvtaadtalyycarentgrtieeig-nffdlwgggtlvt 118
                                                                                                                                                                                                        64 LNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAPSPIKMNÇGPMMLNAFNIWÇQTTLVI 123
                                                                                                     1 llesgpglvkpsetlsltctvsggslssfdw-nwirqpagkqlewigriypsgnthynps 59
                                                                                                                                    4 LLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIYNPS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 553; DB 19; Length 126;
Pred. No. 4.77e-32;
14, Mismatches 25, Indels 2, Cups
                                                                    Saps
                                                                                                                                                                                                                                                                                                                                                                                                 VH of Fab DL 4119, binds to HIV 9p41.
Heavy chain; light chain; variable region; VH; monoclonal antibody; MAD; HIV; human immunodeficiency virus; glycoprotein; gp120; clone; virus infectivity assay; precursor gp160; immunocompetence; human; anti-HIV antibody; detection; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody binding to V1, V2 loop of HIV gp120 - used in
                                                                  Ċ
                             Score 553; DB 10; Length 126; Pred No 4 776-72.
                                                                  Indels
                                                                Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-1995, U08743.
18-JUL-1994, US-276852.
(SCRI ) SCRIPPS RES INST.
Barbas CF, Burton DR, Lerner RA;
                                                                                                                                                                                                                                                                                                                                                 W01315 standard; Protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%;
Matches 82, Conservative
                               59.88;
                                               Local Similarity 65.78;
nes 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95..110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33. 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 AA;
126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96-179601/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9602273-A1.
                                                                                                                                                                                                                                                                                                                                                                                29-JAN-1997
VH of Fab DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
/label = CDR3
                                                                                                                                                                                                                                           119 vss 121
                                                                                                                                                                                                                                                                             124 VSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- CDF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- CDR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label = FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= FR4
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Seguence
                                 Query Match
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                                                                  Matches
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NAME OF THE PROPERTY OF THE PR

1 llesgpglvkpsetls1tctvsggslssfdw-nwirgpagkglewigriypsgnthynps 59

g o

4 LLESGPGLVKPSGTLSLTGTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIYNPS 63

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Monoclonal antibody, MAD; envelope, glycoprotein, gpl20, HIV, AIDS;
CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represents a naturally occurring polyreactive antibody which binds to many antigons. Ab26 shares greatest sequence similarity with germline VN = 71-4.
20 gyglgesgpglykpsetlsltetvsggsv-ssyywswirgppgkglewigyiyysgstny 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-AUG-1995 (first entry)

Human immunoglobulin variable heavy chain #52.

Primer: PCR, amplify, human: immunoglobulin, variable, heavy chain, cosmid; placenta; vector; pIBBl; E.coll; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vh 71-4 gene (042697).
Ab26 (042702) was derived from CD5· B cells of a healthy donor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 64; 109pp; English.
The nucleotide sequence of rearranged F105 Vh (942698) was compare to two monoclonal antibodies (Ab26 · 942702) and 268·D · 942703), which by nucleotide sequence analysis, appear to use a rearranged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA segments encoding menoclonal antibody - which binds to gp120 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 550; DB 7; Length 116; Pred. No. 8 04e-32; 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sodroski JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 npslksrvtisvdtskngfslklssvtaadtavyydar 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-DEC-1992; U10928.
10-DEC-1991; US-804652.
IO-DNU) DANA PAPERP CANCEP INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haseltine WA, Marasco WA, Posner MP, WPI; 93-214174/26.
N-FSDB; Q42697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           chain; epitope; immune deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 12
R66346 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                         R42689 standard; Protein; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 78 6%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                      01-NOV-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20..116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49..54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WC9426895-A
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ID RE
AC AC
DT 04
DE HA
KW P1
KW 72
OS H9
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and graft-versus-host disease.

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Monkey monoclonal antibody binding human B7.1 or B7.2 antigen monkey monoclonal autoimmune disease or graft-versus-host disease useful for treating autoimmune disease or graft-versus-host disease claim 14; Fig 10B; B1pp; English.

Corms of the light and W01821 respectively comprise primatised b7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and b7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and chavy chain constant region genes to allow prodn. of the primatised antibodies have also been produced (see also W01817-20). The antibodies have also been produced (see also W01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 qvqlqesgpglvkpsetlsltctvsggsv-ssyywswirqppgkglewigyiyysgstny ^{78}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-1997 (first entry)
25-MAY-1997 (first entry)
Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
Monoclonal antibody: Cynomolgus monkey: macaque: 16C10;
primatised antibody: B7 antigen; CD28; immunosuppressive:
autoimmune disease; idiopathic thrombocytopaenia purpura;
systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
type 1 diabetes mellitus; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brams P, Hanna N, Shestowsky WS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 npslksrvtisvdtsknqfslklssvtaadtavyycar 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 550; DB 12;
Pred. No. 8.04e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W01822 standard; Protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.5%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 78.6%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-1996; U10053.
07-JUN-1995; US-487550.
(IDEC-) IDEC PHARM CORP.
                                                                                      (NISB ) JAPAN TOBACCO INC
24-NOV-1994.
10-MAY-1993; J00603.
10-MAY-1993; WO-J00603.
                                                                                                                         Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97-108638/10.
                                                                                                                                                   95-006791/01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9640878-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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New New Notation (Notation Figure 1) and the standard form the production of human immunoglobulin to mammalian hosts

Production of human immunoglobulin in mammalian hosts

Production of human immunoglobulin in mammalian hosts

Production of human immunoglobulin heavy chain

Production squences (R66295-51) are novel human immunoglobulin heavy chain

C sequences encoded by novel isolated genes. The genes (078839-79002) were

C solated and cloned from a series of cosmid constructs. 1202; 1103; 721;

C Sisolated and cloned from a series of cosmid constructs. 1202; 7103; 721;

C Sisolated and cloned from a series of cosmid constructs. 1202; 7103; 721;

C Sisolated and cloned from a series of cosmid constructs were isolated from the product weight DNA from human placenta. The DNA was partially considered with Tagl restriction enzyme. The fragments were separated by a cidested with clal-digested and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The VH genes and the consumption human hosts.

S sequence 118 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 qvqlqesgpglvkpsetlsltctvsgqsvssgsyywswirqppqkglewigyiyysqstn 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLLESGPGLVKPSGTLSLTCTVSGGSTRS-SHWWSWVRQPPGKGLEWIGEVFFSGST1 59
                                                                                                                                                                                              80 ynpslksgytistdtskngfslklnsmtaadtavyyevrdrlfsvvg-mvynnwfdvwgp 138
                                                                                                                                                                                                                                  60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNGGRMMLDA-FDIWGO 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
59.4%; Score 549; DB 12; Length 118;
Best Local Similarity 77.8%; Pred. No. 9.57c-32;
Matches 77; Conservative 10; Mismatches 11; Indels 1; Gaps
                                                                                                          20 qvqlqesgpglvkpsetlsltcavsgqsisggygwgwirqppqkqlewiqslysssqnty 79
                                                                                                                                                     1 EVQLLESGPGLVKPSGTLSL7CTVSGGSIRSSHWWSWVROPPGKGLEWIGEVFFS-GST1 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-Aug-1995 (first entry)
Human immunoglobulin variable heavy chain #54.
Primer, PCR; amplify; human; immunoglobulin; variable; heavy chain; osnid; placenta; vector; pJB81; E.coli; mammalian.
                                                                      \ Gaps
                             Length 476;
                                                      Pred. No. 8.04e-32;
19; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin rB6B7 heavy chain variable region
                               Score 550; DB 20;
Pred. No. 8.04e-32;
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R66348 standard; Protein; 118 AA.
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                                 Ouery Match
Best Local Similarity 62.5%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NISB ) JAPAN TOBACCO INC.
Honjo T, Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-1993; J00603.
10-MAY-1993; WO-J00603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95-006791/01.
476 AA;
                                                                                                                                                                                                                                                                                             139 gvlvtvss 146
                                                                                                                                                                                                                                                                                                                                      119 GTLVIVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09426895-A
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Sequence
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Attibody containing immunoglobulin heavy chain mutation - with thyroid function stimulating activity
(Jaim 31, Page 14-15; 18pp; Japanese.
WA4536-W24539 represent the immunoglobulin heavy and light chain variable regions isolated from peripheral blood lymphocyte strains. These sequences were isolated from the B6B7 and 101-2 strains of peripheral blood lymphocytes of a Hasedow's disease patient. These sequences are replaced, deleted or inserted into an antibody, to create the antibodies of the invention. The antibodies of the invention have thyroid function antibody can be used in a method to detect autoantibodies which have thyroid function stimulating activity.
Immunoglobulin; variable region; heavy chain; thyrotropin receptor;
thyroid stimulating activity; light chain; Basedow's disease; antibody;
peripheral blood lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 nsslksrvtisvdtsknqfslklssvtaadtavyycaree-rggl-rdfaygmdvwgggt 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 59.2%; Score 548; DB 12; Length 136; Local Similarity 69.2%; Pred. No. 1.14e-31; nes 83; Conservative 12; Mismatches 22; Indels 2; Gaps
                                                                                 Location/Qualifiers
                                                                                                                                                                                  03-JUN-1997.
22-NOV-1995; 328235.
22-NOV-1995; JF-328235.
(EIKE ) ETKEN KAGAKU KK.
WPI; 97-344899/32.
                                                                                                  Peptide 1..19
/note- "signal peptide"
Protein 20..136
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                                                                Homo sapiens.
                                                                                                                                                               J09140386-A.
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Search completed: Tue Feb 24 07:15:06 1998 Job time: 31 secs.

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Release 2 15 John F Gollins, Riocomputing Poscarch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Peb 24 07:11:04 1999; MasPar time 7.28 Seconds 361 213 Million cell updates/sec Pun on:

Tabular output not generated

IKGRYYLENWGQGTLVTVSS 124 >US-08-844-215-5 (1-124) from US08844215.pep 926 1 EVQLLESGGGVVQPGRSLPL. Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot34
1:part1 2 part2 3.part3 4.part4 5 part5 6 part6 7 part7
8:part8 9-part9 10:part10 11-part11

Mean 42.049; Variance 78 185; scale 0 538 Statistics Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	t	Query		!						
. : Q:	Score	Match	Length	DB.	ID	Des	Description	10n	į	Pred. No.
7	700	Τ,	122	'n	HV3G_HUMAN	Ŋ	HEAVY	THAIN V-II	н	2.75e-124
7	619	73.3	121	ď	HV3J_HUMAN	ğ	HEAVY	CHAIN V-II	н	1.15e-119
m	676		122	u-	HV3H_HCMAN	р	HEAVY	CHAIN V-II	Н	5.230-119
4	699	72.2	126	S	HV3K_HUMAN	ğ	HEAVY	CHAIN V-II	Н	1.80e-117
S	636	α.	119	K)	HV3 I_HIMAN	13	HEAVY	CHAIN V-II	Н	3.09e-110
9	610	62.9	119	S	HV3L_HUMAN	ij	HEAVY	CHAIN V-II	Н	
7	298	Ţ.	117	S	HV3C_HUMAN	5	HEAVY	CHAIN PPECUR	·UR	
<b>c</b> c	593	64.0	120	S	HV3E_HUMAN	ij	HEAVY	CHAIN V-II	Н	7.57e-101
6	588	63.5	120	'n	HV3U_HUMAN	SH	HEAVY	CHAIN V-II	н	9 28p-100
10	584	ω,	$^{\circ}$	S	HV3A_HUMAN	ပ္	HEAVY	CHAIN V-III	<u></u>	
11	577		981	S	HV16_MOUSE	B	HEAVY	CHAIN PPEC	dab	296-9
12	575	⊘i	$\overline{}$	Ŋ	HV3N_HUMAN	ΙĞ	HEAVY	CHAIN V-II	1	.23e-
13	570	61.6	T-1	ĸ.	HV2T_HIMAN	ŗ.	HEAVY	THAIN V-111	j.,	4 60e-96
14	563	c.	$\overline{}$	ır.	HV3M_HTIMAN	ij	HEAVY	CHAIN V-II	H	516-
15	554	6	115	ı,	HV3F_HTMAN	51	HEAVY	CHAIN V-III	Н	2 250-92
16	553	59.7	115	iC)	HV3D_HUMAN	16	HEAVY	CHAIN V-II	Н	.70e-
17	551	6	116	S	HV05_CARAIT	Ľ	HEAVY	CHAIN PPECUP	J.	1.00e-91
18	546	σ,		S	HV3P_HUMAN	SI	HEAVY	CHAIN V-II	н	۲,
19	546	6	142	'n	HV01_PAT	ţ.	HEAVY	CHAIN PPEC	0.	1.216-90
20	543	œ	114	ŗ,	HV3B_HUMAN	Ú	HEAVY	CHAIN V-II	III	5.41e-90
21	542	α.	1133	u ·	HV25_MOUSE	5	HEAVY	CHAIN V RE	103	-016
22	542	η. Ο.	800	เก	HV18_MOUSE	Ç	HEAVY	CHAIN V RE	HOG	01

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# ALIGNMENTS

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                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                       Score 679: DB 5; Length 121:
Pred: No. 1.150-119;
18; Mismatches 16; Indels 3, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE: 74125307.
FLORENT G., LEHMAN D., PUTNAM F.W.;
BIOCHEMICSTY 13:2482-2498(1974).
-!- THIS CHAIN WAS ISOLATED FROM A WALDENSTFOM'S MACHASLORULIN PIR; A02052; M3HUGA.
HSSP, P01772; 1FQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (HIL).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.0%; Score 676, DB 5; Longth 122 Best Local Similarity 63.2%; Pred. No. 5.23e-119; Matches 79; Conservative 33; Mismatches 9; Indels Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRROLIDONE CAPBOXYLIC ACID
                                                                      MEDLINE: 79124695.

MEDLINE: 79124695.

CHU Y.-Y.H., LOPEZ DE CASTRO J.A., POLJAK R.J.:

BIOCHEMISTRY 18:553-560(1979).

--- THIS CHAIN WAS ISOLATED FROM AN IGGI MYELOMA PROTEIN.

PIR: A202044. G1HUHL.

HSSP; P01607; 1FGV.
                                                                                                                                                  PYRPOLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 AA; 13166 MW; D68R085E CRC32;
                                                                                                                                                       1 121 121 121 121 8E91B7EC CRC32;
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21.JUL-1986 (REL. 01, CREATED)
21.JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21.JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (GA).
                                                                                                                                                                                             Match 73.3%;
Local Similarity 70.2%;
les 87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                               EUTHERIA; PRIMATES.
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                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.2%: Score 669: DB 5; Length 126: 71.4%: Pred. No. 1.80e-117: Atlive 17; Mismatches 17: Indels
                                                                                                                                                                                                                                                                                 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                   SEQUENCE, AND DISULFIDE BONDS.
MEDLINE: 83289131.
SCHMIDI W.E., JUNG H.-D., PALM W., HILSCHMANN N.:
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 364:713-747(1983).
                                                                                                                                                                                                 MEDLINE; 81072295.

MARQUERT M., DESSENHOFER J., HURFP R., PALM W.;
J. MOL. BIOL. 141:569-391(1980).

J. MOL. 302055; GHUKE,
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
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                     21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE
01-MAR-1992 (REL. 21, LAST ANNOTATI
IG HEAVY CHAIN V-III REGION (KOL).
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2IG2; 12-JUL-89.
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120
126 AA,
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HV3I_HUMAN
P01770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVQLLESGGGVVQPGPSLPLSCAASGPTFSAYGMHWVPQAPGKGLEWVAGIWFFGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 636; DB 5; Length 119;
Pred. No. 3.09e-110;
22; Mismatches 12; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Mismatches 15; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VERIEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                    CHOPDATA; VEPTEBRATA, TETRAPODA, MAMMALIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 610; DR 5; Length 119;
Pred No 1 49e-104
                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARROXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRPOLIDONE CAPROXYLIC ACID.
                                                                                                                                                                                                                             PONSTINGL H., HILSCHMANN N.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1571-1604(1976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
12981 MW, 323A4FE1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 119 119 119 119 AA: 13242 MW: 5703CA8E CEC32;
21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE-UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III PEGION (NIE)
HOMO SAPERNS (HUMAN),
EUKAPYOTA, METAZOA, CHOPDATA; VEPTEBRATA, TETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (BUR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUTNAM F.W., LIGY -S V., LOW T.L.K.;
J. BIOL. CHEM. 254-2865-2874(1979)
PIR: A02056; AlHUBR.
HSSP. POL772; IFGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMUNOGLOBULIN V REGION; GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE (MYELOMA PROTEIN BUR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.9%;
Best Local Similarity 65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 68.7%;
Best Local Similarity 68.5%;
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDAPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
119 1
119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; PRIMATES.
                                                                                                                                            EUTHERIA; PRIMATES.
                                                                                                                                                                                                            MEDLINE; 77070269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79151016.
                                                                                                                                                                                                                                                                                                    DISULFIDE BOND.
MEDLINE: 77070267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 tvss 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TVSS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
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                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | EVQLLESGGGVVQPGPSLPLSCAASGFTFSAYGMHWVPQAPGKGLEWVAGIWFDGSNQYY 60
1 EVALLESSGRÖVVEPRELFLSCAASSFLFRAFCMHWVFQAFGKGLEWVAGIWFDGSNOYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- THIS CHAIN WAS OPTAINED FROM IGM ISOLATED FROM THE SERUM OF A PAIIENI WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (PEL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SECOUNCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-III REGION (BRO).
HOMO SAPIRNS (HUMAN).
ENKARYOTA: REPRACA, CHOPPATA, VEFIEBRATA; TETRAPODA, MAMMALIA, BUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERIEBPATA; TETPAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG BEAVY CHAIN V-II PEGION (VH26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5, Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE: 81101090.
MATTHYSSENS G., RABBITTS T.H.:
PROC. NATL ACAD. SCI U.S.A. 77:6541-6545(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 598; DB 5; L
Pred. No. 6.16e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQ gdsvkgrftisrdnskntlylgmnslraedtavyyca 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 AA: 13227 MW; B404C4F1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 117
117 AA; 12582 MW; 15A21B2A CRC32;
                                                                                                                                                                                                                                    21-JUL-1986 (PEL 01, CPEATED)
21-JUL-1986 (PEL. 01, LAST SEQUENCE UPDATE)
21-JUL-1996 (PEL. 34, LAST ANNOTATION UPDATE)
1C HEAVY CHAIN PPECURSOP V-III REGION (VH26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDSVKGRETVSRDNSRNTLFLOMNSLRPEDTAVYYCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 AA.
                                                                                                                                                                                                       117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.0%; Score 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAPRA J.D., HOPPER J.E.;
IMMUNOCHEMISTRY 13:995-999(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 64.6%;
Local Similarity 81.4%;
les 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J00236; G553412; -.
EMBL; M35415; G553422; -.
PIR; A02047; H3HC26.
HSSP; P01772; IIGM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                         STANDAPD:
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HSSP; P01772; 1FGV.
IMMUNOSLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                             EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
MEDLINE: 77117574.
                                                                                                   116 tvs 118
                                                                                                                                                                                                HV3C_HUMAN
P01764;
                                                                                                                                  121 TVS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HV3E_HUMAN
P01766;
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SEQUENCE
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SEQUENCE
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CONFLICT
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SIGNAL
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVOLLESGGGVVQPGRSLRLSCAASGETFSAYGMHWVRQAPGKGLEWVAGI WFDGSNQY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEINER L.A., LOPES A.D.;
BIOCHEMISTRY 18:4067(1979).
BIOCHEMISTRY 18:40674-4067(1979).
THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE HINGE REGION.
THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN DISULFIDE BONDS.
                                                                    Indels 6; Gaps
                                1 EVOLLESGGGVVQPGRSTRI,SCAASGFTFSAYGMHWVKQAPGKGLEWVAGIWFDGSNQYY 60
               Indels 5: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-101-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-III REGION (TRO).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPONA; MAMMALIA:
                                                                                                                                                                                     21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 03, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 32, LAST ANNOTATION UPDATE)
1G HENY CHAIN V-III REGION (FORB).
1G HENYY CHAIN V-III REGION (FORB).
1G HENYY CHAIN S (HUMAN).
1G HENY CAPIENTA; TETRAPODA; MAMMALIA;
1GUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 588; DB 5; Le
Fred. No. 9.28e-100;
21; Mismatches 17;
      Best Local Similarity 67.2%; Pred. No. 7.57e-101;
Matches 82; Conservative 20; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                     MANUALDHIIN V REGION.

IMMUNGLOBULIN V 120

SEQUENCE 120 AA; 13440 MW; LCGCF5CF CRC32; SEQUENCE
                                                                                                                                                                                                                                                                               MEDLINE: 80020921.
STEINER L.A., GARCIA PARDO A., MARGOLIES M.N.:
BIOCHEMISTRY 18:4068-4080(1979).
                                                                                                                                                                           PRT; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE (MYELOMA PROTEIN TRO).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.8%,
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                             STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                 PIR; A02065; GlHUDB.
HSSP; P01789; 2FGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                   80020920.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 VTVSS 124
                                                                                                                                                                                                                                                                                                                              CRYSTALLIZATION.
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P01762;
                                                                                                                        119 tl 120
                                                                                                                                         118 TL 119
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                HV3U_HUMAN
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Mismatches 17; Indels 6; Gaps
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BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., KAJEWSKY K.,
                                                                                                                                                                                                                                                 1 dydlydgggglykpggslrlsgvasgfsfrdfymswirztpgkglzwysyjggsgstlyy 60
                                                                                                                                                                                                                                                                                1 EVÖLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVROAPGKGLEWVAGIWFFYGSNOYY 60
                                                                                                                                                                                                                    27; Mismatches 23; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V PEGION (MOPC 21).
D SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
10 HEAVY CHAIN PRECURSOR V RESION (MOFC 21) (FPACMENT).
MUS MUSCULUS (MONE).
EUKARYOTA, METAZOA: CHONDATA: VERTEBRATA; TETRAPOIDS: MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 136;
MEDLINE: 76023781.
KRATZIN H., ALTEVUGI F., RUBAN E., KOPIT A., STAROSCIK K.,
HILSCHMANN N.;
                                                                                                                                                                                           Length 122;
                                                                                                                               PYREGLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYAD -> DYAH (IN REF. 2)

DN -> ND (IN REF. 2).

W -> H (IN REF. 2).

Y -> W (IN REF. 2).

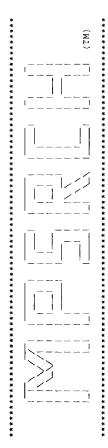
Y -> W (IN REF. 2).

W, 24BFDEBB CRC32:
                                               HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:1337 1342(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.3%; Score 577; DB 5; 1
Local Similarity 68.0%; Pred. No. 2.29e-97;
les 85; Conservative 17; Mismatches 17;
                                                                                                                                                                                            Ouery Match
Best Local Similarity 58.1%; Pred. No. 6.89e-99;
Matches 72; Conservative 27; Mismatches 23
                                                                                                                                                            122 122 13472 MW; BFC0D3D8 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADETUGBO K., MILSTEIN C., SECHER D.S.:
ADETUGB 265:299-304(1977).
EMBL, JO0522: G195055: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15071 MW;
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136
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                                                                                                                            IMMUNOGLOBULIN V REGION.
                                                                                                                                                          122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 ]
136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, A02066; G1MS21
HSSP; P01607; 1FGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 17-136.
                                                                                             PIR; A02045; AlhuTR.
HSSP, F01772; BFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                              77 adtvkgrftisrdnpkntlflqmtslrsedtamyycar---wqny--pyyamdywgggts 131
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1 EVQLLESGGGVVQPGRSLPLSCAASGFTFSAYGMHWVPQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VQLLESGGGVVQPGPSLPLSCAASGFTPSAYGMHWVPQAPGKGLEWVAGIW-FD-GSNQY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gars
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-1- THIS MU CHAIN WAS ISOLATED FROM A WALDFNSTPOM'S MACPOSLOBULIN
PIR; A02064; M3HUGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HILSCHMANN N
                                                                                                                                                                                                                                                                                                                       21-JUL-1996 (REL. 01, CPEATED)
21-JUL-1996 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1996 (REL. 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-III REGION (LAY).
1G HEAVY CHAIN V-III REGION (LAY).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 575, DR 5; Length 119:
Pred No 6 23e-97;
25; Mismatches 13; Indels 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 75046755.
CAPRA J.D., KEHOE J.M.;
PROC. HYLL, ACASCI. U.S.A. 71:4032-4036(1974).
-i- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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WATANABE S , BARNIKOL H !! , HORN J., BERTPAM I , HILS
HOPPE-SEVIER'S Z. PHYSIOL. CHEM. 354:1505-1509(1973).
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119 AA; 12858 MW; 1CE0116C CRC32;
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21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-III REGION (GAL).
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                119 AA
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63 98;
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nes 78; Conservative
                                                                                                                                                                                                                                                                                STANDARD;
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IMMUNOGLOBULIN V REGION.
NON TER 119 119
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PIR; A02058; M3HULY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; PRIMATES.
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                                                                                                                                         132 vtvss 136
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P01775;
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P01781;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 YYSDSVKGRFIVSRDNSRNTLFIQMNSLRPEDIAVYYCATEVLFGSIKGRYYLENWGQGI 118
                                                                                                                                                                                                                                                                     61 vdsvkgrftisrdnaknslylqmnslrvedtalyycarg--wgg--gdy----wqqgtlv 112
                                                                                                                                                                              1 evglvesggdlvqpgrslrlscaasgfbfbblgmtwvrqappgkglewvanikzbgszzby 60
                                                                                                                                                                                                     l evgllesggglvqpggslrlscaasgftfsssamswvrqapgkglewva--wkyengndk 58
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                                                                                                                                   8; Gaps
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (POM).
EURARY CHAIN V-III REGION (POM).
EURARYOTA, METAZOA, CHORDATA, VERIEBRATA; TETRAPODA, MAMMALIA, EURERRAY, PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
MEDLINE; 75046755.
CARRA J.D., KEHOE J.M.;
PROC NATL ACAD SCI U S A 71.4032-4036(1974).
PROC NATL ACAD SCI U S A 71.4032-4036(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKAPYOTA; METAZOA; CHOPDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.8%; Score 563; DB 5; Length 119; 63.4%; Pred. No. 2.51e-94; ative 25, Mismatches 14, Indels
                                                                                  Score 570; DB 5; Length 116;
Pred. No. 7.60e-96;
14; Mismatches 15; Indels
                       116 116
116 AA: 12730 MW: F112826C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA; 12953 MW; DAE69702 CPC32;
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
HOMO SAPIENS (HUMAN).
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                                                                                       Query Match
Best Local Similarity 70.2%;
Matches 87; Conservative
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hes 78; Conservative
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HSSF, P01772; 1FGV.
IMMUNOSLOBULIN V PEGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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IMMUNOCLOBULIN V PEGION.
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                       NON_TER
SEQUENCE
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Pelease 2.1D John F. Collins, Riccomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:11:32 1998; MasPar time 8.34 Seconds 452.970 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-844-215-5 (1-124) from US08844215 PhF 926

1 EVQLLFSGGGVVQPGPSLPL. Description: Perfect Score:

....IKGRYYLENWGQGTLVIVSS 124

PAM 150 Gap 11 Sedneuce.

Scoring table:

95051 seqs, 30469580 residues Searched.

Minimum Match 0% Listing first 45 summaries Post-processing:

pir53 Database:

I abn't 2 ann2 3 ann3 4 ann4 5 unann! 5 unann2 7 unann3 8 unann4 9 udann5 10 udann6 11 unann7 12 udann8 13 unann9 14 unann10 15 unann11 16 unann12 17 unann 18 unnev

Mean 41.610; Variance 126.095; scale 0.330 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Query Match	s Ouery Match Length	DB	GI .	Des	Description	uc		Pred. No.
1	746	0	122	~	സ	Iq	heavy	chain	- hum	
7	720		121	^	S19666	Ϊď	heavy	chain	v req	7
3	719	77.6	C	7	S48797	Ig	heavy	chain	V red	5.10e-78
4	713		133	7	A49028	14	heavy	chain	A-ILI	£.
S	704	9	$^{\prime}$	7	E36005	Ιď	heavy	chain	V req	5.51e-76
9	703	'n.	132	7	S31603	Н	heavy	chain	v red	7
7	700		C1	C.	MSHUAM	Н	heavy	chain	V-III	۲-
α	909		۴.	٢	531674	t t	yveor	chain.	V rea	ŗ
6	695		120	r·	531115	H	heavy	chain	· hum	1
10	663		-1	7	831116	ВI	heavy	chain	- hum	7
11	069		C	7	S36278	Τď	heavy	chain	V red	7
15	689	74.4	( )	7	869910	, p	V .	10.00	` '	7
13	688	74.3	121	~	G36005	Iq	heavy	chain	>	
14	688	74 3	C	7	531598	Iq	heavy	cha in	v reg	8.08e-74
15	989		$\sim$	^	S31510	Ig	heavy	chain	- hum	1
16	584		(1	r.	531104	Ιď	hear	chain	ogns)	2 815-73
17	684	73.9	160	۲-	S05271	+H	heavy	chain	precu	2.81e-73
18	683		$\leftarrow$	7	531111	F	heavy	chain	E	3.840-73
19	683		151	^	A60943	Ιď	heavy	chain	precu	3.84e-73
50	629	73.3	C4	C1	CIHOHI	H	heavy	chain	III.A	1.330-72

1 qvqlvesgggvvqpgrslrlscaasgftfssygmhwvrqapgkglewvaviwydgsnkyy 60 

> St. 성 Ċ q

.490-7	.396.7	.326-7	.63e-7	.62e-7	.19e-7	.00e-7	4.09e-71	.u9e-7	.94e-7	.94e-7	. 540-7	.64e-7	.71e-7	.71e-7	.15e-7	.25e-6	250-6	.70e-6	336-5	336-6	.33e-6	.33e-6	.33e-6	9-006		
q heary chain -	g heavy chair V-	q heavy chain V	g heary o	g heavy chain .	g heavy chain V r	q heavy chain V-I	heavy	g heavy chain V r	g mu chain - huma	g heavy chain V-D	g heavy chais V r	g heavy chain V r	g heavy	g mu chain - huma	g heavy chai	g heavy chain V	q heavy chain -	P T	g heavy chain V r	g heavy chain V r	g hea	gM - human (fragm	g heavy chain V re	ig heary chain V reg		
831114	M3HUGA	F36005	\$26993	538493	PH1642	GIHUKI	S20782	Sileul	S37453	S44111	531701	S31588	836259	537455	S38490	535273	S31119	S31107	\$30532	S31586	S48798	I55673	S31679	346295		ALIGNMENTS
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21	C 3	C)	C I	C4 10	97	27	00 C1	67	ЭÜ	31	3.2	33	34	2.5	36	37	38	39	4.0	41	42	43	44	u · *J'		

S31117 #type complete Ig heavy chain - human #formal_name Homo sapiens #common_name man 02-Dec1993 #sequence_revision 26-May-1995 #text_change	S31117 S31107 S31107 F3apphors, F.M.: Timmors, E.; Kenter, M.J.H.; van Tol, M.J.D.: Vossen, J.M.: Schourman, R.K. B. Eur. J. Immorsol (1992) 22:247-251 Restricted utilization of germ.line V(H)3 genes and short diverse third complementarity-determining regions (CDR3) in	human fetal B lymphocyte immunoglobulin heavy chain rearrangements. ##status preliminary; nucleic acid sequence not shown; ##molecule_type mRNA ##residues	##Gross-relerences EMBL:X0.290/ ##note the nuclea sequence was submitted to the EMBL Data Library, October 1991 FTCATION #superfamily immunoglobulin V region: immunoglobulin homology DS heterotetramer; immunoglobulin E #domain immunoglobulin homology #label IMM #length: 122 #molecular-weight 13664 #checksum 8338	Query Match 80.6%; Score 746; DB 7; Length 122; Bost Local Similarity 79.0%, Pred. No. 1.10e-81; Matches 98; Conservative 17; Mismatches 7; Indels 2; Gaps 2;
RESULT 1 ENTRY TITLE OPGANISM DAIE	ACCESSIONS REFERENCE #arthors #journal	#accession ##status ##molecule ##molecule	##CTOSS'R ##note CLASSIFICATION KEYWORDS FEATURE 15-98	Query Match Best Local Si Matches 98

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#authors Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.;
#authors Griffiths, A.D.; Winter, G.
Griffiths, A.D.; Winter, G.
#journal J. Mol. Biol. (1991) 222-581-597
#journal By-passing immunization. Human antibodies from V-gene
#title libraries displayed on phage.
#cross-references, MulD:92085276
                                                                                                                                                                                                                                                                                                   ##cross_references_EMBL:X61646
##cross_references_EMBL:X61046
FICATION #superfamily immunoglobulin v region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVOLLESGGGVVQPGRSIRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFUGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548797 #type complete
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human
#formal_name Homo sapiens #common_name man
#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
        Ig heavy chain v region (VH3DJH4) - human
#formal_name Homo sapiens #common_name man
22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change
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gth 128 #molecular-weight 14474 #checksum 9058
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                                                                                                                                                                                                                                                                                                                                                                           #domain immunoglobulin homology #label IMM #length 121 #molecular-weight 13296 #checksum 9195
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Pred. No. 5.10e-78;
13; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 77.8%; Score 720; DB 7; Length 121; 79.0%, Prod. No. 3.73e-78; Ative 14; Mismatches 9; Indels
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Best Local Similarity 77.3%;
Matches 99; Conservative
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Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.;
Timmers, J.E.; Alt, F.W.; Schuurman, R.K.
Berman, J.E.; Lumucoi. (1991) 21:2355-2363
Bur, J. Lmmucoi. (1991) 21:2355-2363
Diversity of immunoglobulin heavy chain gene segment
rearrangement in B lymphoblastoid cell lines from X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schroeder Jr., H.W.; Wang, J.Y. proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150 proc. Natl. Acad. Sci. U.S.A. (1990) Preferential utilization of conserved immunoclobulin heavy preferential utilization of conserved immunoclobulin heavy chain variable gene segments during human fetal life.
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Igheavy chain'v region (M72) - human
Aformal name Homo Sapiens #common_name man
21-Dec-1990 #sequence_revision 21-Dec-1990 #tovt_change
61 SDSVKGRETVSPNNSRNTLFLQMNSLRPEDTAVYYCATEVLFGSIKGRYY----LENWGO 115
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#formal_name Homo sapiens #common_name man
21-Jan-1994 *sequence_revision 18-Nov-1994 *text_change
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#length 133 #checksum 8516
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Matches 96; Conservative
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           *superfamily immunoglobulin V region; immunoglobulin hamalogy heterotetramer; immunoglobulin
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                                                                                                                                           4; Gaps
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Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver. $31603
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Ig heavy chain V-III region (Cam) - human
#formal_name Home sapiens #common_name man
31-Aug-1980 #soquence_revision 22-Oct-1981 #text_change
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Iq heavy chain V region - human
*formal_name Homo sapiens *common_name man
03-Mar-1994_*sequence_revision 10-Nov-1995 *text_change
                                                            #domain immunoglobulin homology #label IMM
gth 122  #molecular weight 13527 #checksum 630
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                                                                                                           Length 122;
                                                                                                        Score 704; DB 7; Length 122;
Pred. No. 5.51e-76;
16; Mismatches 8; Indels
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Pred. No. 7.53e-76;
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##cross-references GB:M34030
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##residues
                                                                                                           76.38;
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Best Local Similarity 77.6%;
Matches 97; Conservative
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##cross-references GDR-128528
#map_position 14q32.33-14q32.33
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
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FICATION *Supertamily immunoglobulin V region; immunoglobulin homology
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#authors Lehman, D.W.; Putnam, F.W.
#jornal Proc. Natl. Acad. Sci. U.S.A. (1988) 77-3239-3243
#title Amino acid sequence of the variable region of a human mu chain: location of a possible J-H segment.
#cross-references WUID:81013859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tonnelle, C.
submitted to the EMBL Data Library, June 1992
Mechanisms that generate human immunoglobulin diversity
operate from the 8th week of gestation in feral liver.
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22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
16-Aug-1996
                                                                                                                                                                                                                                                                                       This mu chain was isolated from the plasma of a patient with
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#length 122 #mclecular.weight 13568 #checksum 7281
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Ig heavy chain V region - human (fragment)
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Eur. J. Immunol. (1992) 22:247-251
Restricted utilization of germ-line V(H)3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte immunoglobulin heavy chain
                                                                                                                                                                                                                                                                                           Raphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
Eur. J. Immunol. (1992) 22:247-251
Restricted utilization of germ-line V(H)3 genes and short diverse third complementarity-determining regions (CDR3) in human feal B lymphocyte immunoglobulin heavy chain
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Library, October 1991
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#formal_name Homo sapiens #common_uame man
02-Dec-1993 #sequence_revision 26-May-1995 #text_change
4; Gaps
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#formal_name Homo sapiens #common_name man
02-Dec-1993 #sequence_revision 26-May-1995 #text_change
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##residues 1-120 ##label RAA
##cross-references EMBL:X62961
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##residues 1-120 ##label GRI
##residues 1-120 ##label GRI
##cross-references EMBL:218830
FICATION #superfamily immunoqlobulin V region; immunoqlobulin homoloqy
DS heterotetramer; immunoqlobulin
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Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
                                                                                                             *superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin
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Human anti-self antibodies with high specificity from phage
display libraries.
##residues 1-118 ##label RAA
##cross-references EMBL:X62966
##note the nucleotide sequence was submitted to the EMBL bata
##note the nucleotide sequence was submitted to the EMBL bata
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                                                                                                                                                                                                                                                                     74.8%; Score 693; DB 7; Length 118;
79.0%; Pred. No. 1.70e-74;
ative 15; Mismatches 5; Indels 6; Gaps
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03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996
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#length 118 #molecular-weight 12778 #checksum 4374
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74.5%; Score 690; DB 7; 1
Best Local Similarity 73.2%; Pred. No. 4.33e-74;
Matches 90; Conservative 18; Mismatches 12;
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Matches 98; Conservative
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118 tvss 121 |||| |21 TVSS 124

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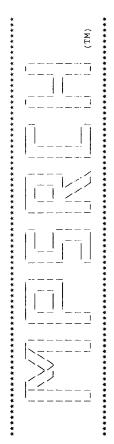
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the sequence of residues 108-122 and the corresponding nucleic acid sequence are not shown sequence are not shown superfamily immunoglobulin V region; immunoglobulin homelogy #length 122 #molecular-weight 13511 #checksum 583
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*journal Proc Natl Acad Sci. U.S.A. (1990) 87:5146-5150

*title Preferential utilization of conserved immunoglobulin heavy chain variable gene segments during human fetal life.

*cross-references MUID:90349571
                                                                                                                                      Sahota, S.; Hamblin, T.; Oscier, D.G.: Stevenson, F.K.
Leukemia (1994) 8:1285-1289
Assessment of the role of clonogenic B lymphocytes in the
pathogenesis of multiple mycloma.
869910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Mismatches 12; Indels 4; Gaps
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Ig V-D-J region (KR) - human
#formal_name Homo sapiens #common_name man
14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
09-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G36005 #type complete
Ig heavy chain V region (M74) - human
#formal_name Homo sapiens #common_name man
21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
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                                                                                                                                                                                                                                                          preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 122;
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Pred. No. 5.92e-74;
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##cross-references EMBL:233400
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**cross-references GB:M34031
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Best Local Similarity 75.2%;
Matches 94; Conservative
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Best Local Similarity 77.4%;
Matches 96, Conservative
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##residues 1-135 ##label CUI ##residues CII-135 ##label CUI ##residues CII-135 ##label CUI ##cross-references EMBL:314170 CLASSIFICATION ##superfamily immunoglobulin V region: immunoglobulin homology KEYWORDS heterotetramer; immunoglobulin
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##cross-references EMBL:X69865
FICATION *superfamily immunoglobulin V region, immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 adsvkgriftisrdnsknilylgmnslraedtavyycak-iswe-v-sri--dywggqilv 131
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                                                                                                                                                                      Cuisinier, A M . Gauthier, L . Roubli, I., Fougereau, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17. gyglvosgggyvgpggslrlschasgftfssygmhwyrgapgkglowyafirydgsnkyy 76
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      Tonnolle, C. submitted to the EVBL Data Library, Jane 1992
Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver 831598
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#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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74.1%; Socre 686; DB 7; Length 133
Best Local Similarity 76.4%; Pred. No. 1.51e-73;
Matches 94, Conservative 17, Mismatches 10, Indexs
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77 48; Pred. No. 8 08e-74;
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Release 2 1D John F. Collins, Biocomputing Pesearch Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.R. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Reb 24 07 39 16 1998, MasPar time 3.55 Seconds 177-836 Million cell updates/sec Tabular output not generated. Pun on.

>US-08-844-215-5 (1-124) from US08844215.pep 926 1 EVQLLESGGGVVQPGRSLRL. Description: Perfect Score: Sequence:

IKGRYYLENWGQGTLVTVSS 124

PAM 150 Gap 11 Scoring table:

56402 segs, 5095871 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:backl 2-51 3-52 4-53 5-54 6-55 7-56 8-pcrg0 9-pcr91 10-pcr92 11-pcr93 12-pcr94 13-pcr95 14-pcr96

Mean 28.178; Variance 148 297; scale 0.190 Statistics: Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

## SUMMARIES

		*					
Result No.	Score	Query Match	Query Match Length D	DB	QI QI	Description	Pred. No.
		11111		1			
1	695	75.1	11	7	US-08-331-		1.07e-45
C3	687	74.2	ä	7	US-08-478-	99,	4.640-45
m	684	73.9	Н	۲-	US-07-942-	(n)	00)
4	683	73.8	] 4	Ç,	US-08-259-	2, 2	œ.
5	683	73.8	14	7	US-08-468-	2	σ.
9	682	73.7	125	11	PCT-US93-1	ř	П
7	674	72.8	11	11	PCT-US93-0	43,	Ŋ.
80	672	72.6	122	덛	PCT-US93-0	14,	۲-
6	670	72.4	122	11	PCT-US93-0	Sequence 12, Applicati	
10	099	71.3	125	7	US-07-942-	33,	6.59e-43
11	099	71.3	142	7	US-08-305-	c i	6.590-43
12	658	71.1	CC	r-1	PCT US93-0	d	c,
13	657	71.0	123	۲	-874-80-8U	70	
14	655	707	116	œ.	US-08-211-	Sequence 141, Applicat	<del>(- 1</del>
15	654	70.6	125	11	PCT-US93-1	9	H
16	654	70.6	125	11	PCT-IIS93-1	r.	1.986
17	646	6. B	e 6	v.	-112-60-Si	급	α,
18	640	69.1	117	7	US-07-942-	36,	c.i
19	640	69.1	130	7	US-08-478-	63	2 5Re
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21	637	68.8	119	12	PCT-IIS94-0	Sequence 6 Applicatio	4.470-41
13	537	98	1. P. C. I.	۲.	P2T-T895-0	C	4 470-43

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RESULT
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARR----SART-YYFDYWGQGTLV 115
                                                                                                                                                                                                                                               1 QVELVESGGGVVQPGPSLPLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
                                                                                                                                                                                                         Score 695; DB 7; Length 119;
Pred. No. 1.07e-45;
14; Mismatches 8; Indels 5, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
                                                                                                                                R INFORMATION: 55P1'CL Variable Heavy chain (V-H)" 119 AA: 13279 MW; 79818 CN:
                                                                                                     LUCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin OTHER INFORMATION: 56P1/CI. Variable "...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA A
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JHN-1995
                                                                                                                                                                                                                                                                                                                               125 AA.
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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/375,072 FILING DATE: 25-3AN-1995 PRIOR APPLICATION DATE: US 07/912,292 APPLICATION NUMBER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JMBER: US 07/912,292
10-JUL-1992
                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 99, Application US/08478039
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 99, Application US/08478039.
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEO ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READARLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPIOP APPLICATION DATA:
                                                                                     MOLECULE TYPE: protein
                                                                                                                                                             Query Match
Best Local Similarity 78.2%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexandria
                                                           amino acid
                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                   STRANDEDNESS:
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                                                                               TOPOLOGY:
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STATE:
                                                                                                                                                                                                                                                                          116 TVSS 119
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                                                                                                                                             SEQUENCE
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ID US
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61 ADSVKGRFIISRDDSKNTLYLQMNSLRAEDTAVYYCAKGQVLYYG-SGSYHWFUPWGGGT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Michael A.
Braydon C.
SURFACE RESIDUE VENEERING OF HODENT
ANIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seds
STREET: 2100 Pensylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                              Score 687; DB 7;
Pred. No. 4.64e-45;
                                                                                                                                                      012712-160
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HP 9000/700 Workstation
                                                           us 07/735,064
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                75 97/856,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
                                                                                                                                                                                                                                                                                                                                                                CHROMOSOME/SEGMENT: 18/2
NCE 125 AA, 13543 MW, 93321 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 35, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/07942245.
                                                                                                                                   35,030
                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                  NAME: Teskin Esq., Robin L. REGISTRATION NUMBER: 35,030
                         FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/7
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               not relevant
                                                                                                                                                                                                             TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 99:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDAPD;
                                                                                                                                                                                                                                                            : 125 amino acids
amino acid
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20037-3202
                                                                                                                                                                                                                                                                                                                not relevant
                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              LECOMBER 703-8
TELEFHONE: 703-836-2021
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                                                                                                                                                                                                                                                                                                                 TOPOLOGY: not relevan
MOLECULE TYPE: peptide
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 73.8%;
les 93; Conservations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA: AFFLICATION NUMBER (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROGUSKA, PAPPLICANT: ROGUSKA, PAPPLICANT: GUILD, ITITLE OF INVENTION: STITLE OF INVENTION: AN UNMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In house
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SOFTWARE: In hous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 LVTVSS 125
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afent No. 55460...
GENERAL INFORMATION:
APPLICANT: OSTBERG, LAIS G.
ATILE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPAIITIS B SUPFACE ANTIS
                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVPQAPGKGLEWVAGIWFPGSNQYY 60
                                                                                                                                                                                                                                                                                                                                    4, Gaps
                                                                                                                                                                                                                                                                                                              Length 141;
                                                                                                                                                                                                                                                                                                           Chery Match 73.8%; Score 683; DB 6; Length 141 Best Local Similarity 77.6%; Pred. No. 9.67e-45; Matches 97; Conservative 10, Mismatches 14, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTEP - IRM PC COMPATIBLE
OPERATING SYSTEM: POTENS FOR
SOFTWARE: PALENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFFESPONDENCE ADDRESS:
ADPRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CIII: San Francisco
                                                                                                                                              NAME: Smith, William M.
PFOTETRATION NUMBER: 30,223
PFFERENS/COCKET NUMBER: 11823-50-7
TELECOMMINICATION INFORMATION:
      APPLICATION NUMBER: US 07/538,796
FILLNS DATE: 15-HN-1940
PRIOR APPLICATION DATA:
                                                            PRIOR APPLICATION DATA
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-0cT-1986
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 06/904,517
                                         us 07/192,754
                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 141 AA: 15613 MW; 114738 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08468671.
                                                                                                                                                                                         TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      11-MAY-1988
                                                                                                                        05-SEP-1986
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                        APPLICATION NUMBER.
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                                                    FILING DATE:
                                                                                                                        FILING DATE:
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IIILE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
IIILE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPAIIIIS B SURFACE ANTIG
                                                                                                                                                                                                                                                                                                  61 ADSVKGPFTISPDNSKNTLYLQMNSLRAEDTAVYYGAPDPK-DW--GWALFDYWGQSTLV 117
                                                                                                                                                                                                                                                     Match 73.9%; Score 684; DB 7; Length 120; Local Similarity 77.2%; Pred. No. 8.05e-45; es. 95; Conservative 14; Mismatches 11; Indels 3; Gaps
                                                                                                                                                                                                                                        1 QVQLVESGGGVVQPGPSLPLSCAASGFTFSSYAMHWVPLAP4KGLEWVAVISYfwtSNKYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1 0, Version #1 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 16
COPPESPONDENCE ADDRESS.
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                        141 AA
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FILING DATE: 21-APR-1992
APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER- US 07/676,036
27-MAR-1991
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                                                                                                                                                      MOUSCULE TYPE: peptide
ENCE 120 AA, 13421 MW, 78517 CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08259372A Patent No. 5565354 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/98259372A.
                                                            TELEPHONE: (202) 293.7060
TELEFAX: (202) 293.7860
TELEX 6491103
INFORMATION FOR SEQ ID NO. 35.
SEQUENCE CHARACTERISTICS.
LENGTH: 120 mains acids
TYPE: amino acid
TOPOLOGY: linear
                                       CLASSIFICATION 530
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                        STANDAFL
       CURRENT APPLICATION DAIA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834
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                              FILING DATE:
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US-08-259-372A-2
                                                                                                                                                                                                                                                                                                                                   118 TVS 120
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                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                           Query Match
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NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                 FILING DATE:
                                                                                                   MEDIUM TYPE:
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                                                                           90067
                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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APPLICANT:
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APPLICANT:
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                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                      LENGTH:
                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 ADSVKGRFTISRDNSKNTLFLQMHSLRAADTGVYYCAKDQLYFGSQSPGHY----WVQGTL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSPYGMHWVPQAPGKGLEWVAVISYDGSNKWY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 9.67e-45:
10; Mismatches 14; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 683; DB 7; Pred. No. 9.67e-45:
                                                                                                                                                                                                                                                                                           11823-50-7
                                                                                                                                                                                                  APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904.517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
                                                                                       FILLING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FTI.ING DATE: 27-MAR-1991
                                                                                                                                   APPLICATION NUMBER US 07/538,796 FILING DATE: 15-JUN-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/192,754 FILING DATE: 11-MAY-1988
                                                                    UMBER: US 07/871,426
21-APR-1992
     APPLICATION NUMBER: US/08/468,671
                                                  US 08/259,372
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 141 AA; 15613 MW; 114738 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9310555
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application PC/TUS9310555.
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THEREOF
                FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 14-JUN-1994
                                                                                                                                                                                                                                                                                                                                                        : 141 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD,
                                                                                                                                                                                                                                                                      NAME: Smith, William M.
REGISTRATION NUMBER: 30
                                                                                                                                                                                 FILING DATE: 11-MAY-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 31-OCT-1
                                                                                                                  FILING DATE: 27-MAR-1
PPIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 15-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 77.6%;
Les 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          73.8%;
                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                  FILING DATE:
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Novel Antibodies for Conterring Passive
Immunity Against Infection by a Pathogen in Man
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPCKGLEWVSAISGSGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.7%; Score 682; DB 11; Length 125; Best Local Similarity 73.8%; Pred. No. 1.16e-44; Matches 93; Conservative 18; Mismatches 12; Indels 4; Gaps
                                                                                                                                                                                                                                               SOFTWARE: Patentin Ralease #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION UNBER: PCT/IIS93/10466
ALESSEE: Spensley Horn Jubas & Lubitz
EET: 1880 Century Park East - Suite 500
(: Los Angeles
E: California
"RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Government, Secretary of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U. S. Government, Secretary of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DUS/MS-DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ION: 1..125
125 AA; 13464 MW; 94507 CN;
                                                                                                                                                                                                                                                                                                                                                                                               MAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET UNMBER: FD-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                    29-0CT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: Si
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01-JAN-1900
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  APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the APPLICANT THREE OF INVENTION: Immunity Against Infection by a Pathogen in Man CUMPRER OF SEQUENCES: 61
COPPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PDTVTGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASLIYYG-YDG-YAMDYWGQGTLV 118
                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVAEISLGGGSYTYY 60
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                                                                                                                                                                                                                                                                                                                                                                               Caps
                                                                                                                                                                                                                                                                                                                                                        Ouery Match 72.8%; Score 674; DB 11; Length 122; Best Local Similarity 75.0%. Pred. No. 5.05e-44; Matches 93; Conservative 14: Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Felease #1.0, Version #1.25
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SmithKline Reecham, Corporation APPLICANT: U. S. Government, Secretary of
                    Howson and Howson
x 457, 321 Norristown Road
                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: SEC P50107 TELECOMMUNICATION INFORMATION
                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA-
APPLICATION NUMBER: US 07/941,654
FILING DAIE: 09-5EP-1992
ATTORNEY/AGENT INFORMATION-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application PC/TUS9308435 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 122 AA; 13313 MW; 87403 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application PC/TUS9308435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Howson and Howson
                                                                                                                                                                                                               NAME: Bak, Mary E. PEGISTRATION NUMBER 31,215
                                                                                                                                                                                                                                                   TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                : 122 amino acids
amino arid
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                              COMPUTER READARLE FORM.
                             STREET: Box 457, 32
CITY: Spring House
                                                                                                                                                                                                                                                                                                                    linear
                                                          USA
                                                                  19477
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PCT-US93-08435-14
                     ADDRESSEE:
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                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
TITLE OF INVENTION: Novel Antibodies for Conferring Passive
NUMBER OF SEQUENCES: 61
MAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SDSVKGPFTVSPDWSPNTLFLQMNSLPPEDTAVYYCATRVLFGSIKGRYYLENW3GGTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVULLESGGGLVQPRASIRISGAASAFTFSSYAMSWVPQAPGKGLEWVSEISDGGSYTYY 50
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                                                                                                                                                                                   OPBPATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Pelease #1.0, Version #1.25
GURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/NS03/08435
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ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
  Box 457, 321 Norristown Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMINICATION INPOPMATION:
TELEPHONE: (215) 540-9200
TELEFA: (215) 540-5818
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
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JENCE 122 AA; 13329 MW; 88138 CN;
                                                                                                                                                               COMPUTER: IBM PC compatible
                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 122 amino acids
amino acid
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
STREET: Box 457, 32
CITY: Spring House
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                                                                                                                                                                                                                                                                                                                                        1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSEISDGGSYTYY 60
                                                                                                                                                                                                                                                                                                                                                             1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                       Gaps
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Michael A.
Braydon C.
SURFACE PESIDUE VENEERING OF PODENT
                                                                                                                                                                                                                                                                                               Query Match 72.4%; Score 670; DB 11, Length 122; Best Local Similarity 74.2%; Pred. No. 1.05e-43; Matches 92; Conservative 14; Mismatches 16, Indels
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STREET: 2100 Pensylvania Avenue, N W
CITY: Washington
STATE: D.C
                   COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRIY APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
                                                                                                                                                               REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMOUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 12:
                                                                                                   CLASSIFICATION.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-5EP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FINCE 122 AA, 13370 MW, 87746 CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stephen M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33, Application US/07942245 Patent No. 5639641 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application US/07942245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PEDERSEN, Jan T. APPLICANT: SEARLE, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: United States 20037-3202
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: REES, AND APPLICANT: ROGUSKA, MICA APPLICANT: GUILD, BET ITLE OF INVENTION: SURFILLE OF INVENTION: ANT NUMBER OF SEQUENCES: 522 CORRESPONDENCE ADDRESS:
                                                                                                                                                      Bak, Mary E.
                                                                                             FILING DATE:
           19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-942-245-33
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61 ADSVKGPFTISPNDSKNTLFLQMDSLPPEDTGVYFCARPGGHGFCSSASCFGPDYWGQGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LAKE, Philip
APPLICANT: LAKE, Bribara
APPLICANT: OSTREG, Barbara
APPLICANT: OSTREG, LAYER
TITLE OF INVENTION: MONOCLONAL, ANTIRONY TO HERPES SIMPLEX
TITLE OF INVENTION: VIPUS AND CFIL LINE PRODUCING THE SAME
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 660; DB 7; Length 125; Pred. No. 6.59e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 17, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 AA.
                                                                                                               USEP-1992
                   MEDIUM TYPE: Floppy disk
GOMPHTER: HP 9000/700 Workstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
JENCE 125 AA; 13631 MW; 85784 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PS/08305683A Patent No. 5646041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08305683A.
                                                                                                                                                         CLASSIFICATION: 53.0F 1772
CLASSIFICATION: 53.0
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 293-7060
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENTH: 125 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: HARFELDT, Elisabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COPPESPONDENCE ADDRESS:
ADDRESSEE: Townsend and TC STREET: 379 Lytton Avenue CTTY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                           OPERATING SYSTEM: UNIX
                                                                            SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 69.6%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
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                                                                                                                                              FILING DATE:
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US-08-305-683A-2
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80 GESVKGPFIISPDNSKNILYLQMNSLPAEDTAVYYCAPGG-YG--PGHYFYGLDVWGPGT 135
                                                                                                                                                                                                                                                                                                                        20 QVQLVESGGGVVQPGRSLPLSCAASGFTFSSHVMHWVPQAPGRGLGWLAVTWYPGSNKAY 79
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                              / Match
Local Similarity 71.3%; Score 560; DB 7; Length 142;
Local Similarity 71.8%; Pred. No. 6.59e-43;
les 89; Conservative 17; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 5 25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
                                                                      11823-005230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 460 Point San Bruno Blvd CITY: South San Prancisco STATE: California COUNTY: USA ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JMBER PCT/US93/07832
19930820
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            US 07/759,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application PC/TUS9307832
                                                                                                                                                                             MOLECULE TYPE: protein
JENCE 142 AA; 15758 MW, 111669 CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application PC/TUS9307832
                                           NAME: Liebeschuetz, Joe
REGISTRATION NUMRER: 37, 505
REFERENCE/DOCKET NUMRER: 11923
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 26-2400
TELECOMMUNICATION 00: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                     FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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PRIOR APPLICATION DATA APPLICATION NUMBER.
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GENERAL INFORMATION:
APPLICANT: Genenti
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                                                                                                                                                                                           SEQUENCE
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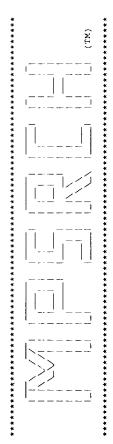
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7
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                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAASGFIFSSYAMSWVRQAPGKGLEWVSVISGLGGSTYY 60
                                                                                                                                                                                                                                  Indels 4. Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Razb, Ronald W.
ITILE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
                                                                                                                                                                         Match 71:18, Score 658, DB 11, Length 122, Local Similarity 75:28; Pred. No. 9:51e-43; es 94; Conservative 15, Mismatches 12, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                          123 AA
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APPLICATION NUMBER: (%,070,072
FILING DATE: 25-JAN-1995
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APPLICATION NUMBER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                                                           FPT;
                                                                                                                                             LOGY: linear
122 AA: 13077 MW: 86439 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 94, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 94, Application US/U8478039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
                                          PEFERENCE/DOCKET NUMBER: 70
TELECOMMINICATION INFORMATION:
                                                                          TELEFAX: 415/952-9881
TELEEX: 910/331-7168
INFORMATION FOR SEQ ID NO. 21:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTPY: USA
21P: 22313-1404
COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0-JUL-1992
                                                                                                                       LENGTH: 122 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                           STANDAPD:
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                                PEGISTPATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria STATE: VA
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US-08-478-039-94
                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                            118 VTVSS 122
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                       NAME
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ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                        61 SDSVKGFFTVSFDNSRNTLFLOMNSLRPEDTAVYYCATE-V-LFGSIKGRYYLENWGQGT 118
                                                                                                                                                                                                                                                                                                                                                                                             61 ADSVKGRFTISRDDSNNTLYMGMNSLRAEDTAVYYCARDRVAVYASVFFIDSFDIWGQGT 120
                                                                                                                                                                                                                                                                                                                                                          1 EVOLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGTWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                              1 QVQLVESGGGVVQPGFSLFLSCAASGFTFSSYGMHWVRQAPGKGLEWVXVISYDGSNEYF 60
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BAIER, Michael APPLICANT: BAIER, Michael APPLICANT: BESPERS, Laurent Stephane Anne Therese APPLICANT: WINTER, Gregory Paul TITLE OF INVENTION: Production of chimeric antibodies - TITLE OF INVENTION: combinatorial approach NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                    Score 657; DB 7; Length 123;
Pred. No. 1.14e-42;
19, Mismatches 13: Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6300 Sears Tower, 233 South Wacker Drive
                                                                                    REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEBRONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRT;
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07.73E ^^^
                                           APPLICATION NUMBER: US 07/735,064 FILING DATE: 25-JUL-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 141, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
                                                                                                                                                                                                                                 MOLECULE TYPE. peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: RF TS2
JENCE 123 AA; 13515 MW, 82958 CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 141, Application US/08211202.
                                                                                  NAME: Teskin Esq., Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                          INFORMATION FOR SEQ ID NO: 94: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          is: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                   LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                             Query Match 71.0%;
Best Local Similarity 72.4%;
Matches 89; Conservative
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60606-6402
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US-08-211:202-141
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STIVEPMAN, GREGG J.
JENTION - METHOD FOR STIMULATING PRODUCTION OF
JENTION: VARIABLE PEGION GENE FAMILY RESTRICTED ANTIHODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VACCINATION WITH A P-CELL SUPERANTIGEN AND CONJUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .:.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVESGGGVVQPGPSLPLSCAASGFTFSSYAMHWVPQAPGKGLEWVAVISYDGSNKYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SUSVKGPFTVSPDNSPNTLFLØMNSLPPEDTAVYYCATEVLFGSIKGRYYLENWGQG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 655; DR 6; Longth 116;
Pred No 1 65e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 12; Indels
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1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 AA
                                                                                                                                                                                                                                                                                                                                                                                                           28111/31960
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/GB92/U0883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: anim...
TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE 115 AA; 12678 MW, 72426 CN;
APPLICATION NUMBER, US/08/211,202
FILING DATE: 23.SEP-1992
CLASSIFICATION: 435
                                                                                                                                                        FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
                                                                                                                                                                                                                FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR DATE: APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/0088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                            APPLICATION NUMBER: GB 9120252.3 FILING DATE: 23-SEP-1991
                                                                                                                                   GB 9120377.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application PC/THS9310555 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELERAX: 312-474-0448
TELEX: 29-3856
INFORMATION FOR SEQ ID NO: 141:
                                                                                                                                                                                                                                                                                                                                                                                             36,107
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 116 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          David W. Clough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION THI
NUMBER OF SEQUENCES 5:
COPRESPONDENCE ANDRESS:
                                                                                                FILING DATE: 23-SEP-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76 1%;
watches 89; Conscrvative
                                                                                                                                                                                                                                                                                                                                                                                           PEGISTRATION NUMBER.
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California
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PCT-US93-10555-6
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1 EVQLVESGGGVVQPGSSLRLSCAASGFTFSSFAMHWVRQAPGKGLEWVAVMSYSGDNKYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 70.6%; Score 654; DB 11; Length 125; Local Similarity 72.0%; Pred. No. 1.98e-42; nes 90; Conservative 15; Mismatches 19; Indels 1; Gaps
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: HOWells, Stacy L.
REGISTRATION NUMBER: 34,842
PREFRENCY/COCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPAN: (619) 455-5100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 aming acids
                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide
LOCATION: 1..125
SEQUENCE 125 AA; 13612 MW; 90692 CN;
                                                                                                                                                                                                                                                   STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: RIV
                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VTVSS 125
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                                                                                                                                                                                                                                                                                                                    FEATURE:
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Matches
   QC
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Search completed: Tue Feb 24 07:39:21 1998 Job time : 5 secs.



Release 2.1D John F. Collins, Biocomputing Pesserch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:12:31 1998; MasPar time 7:36 Seconds 234.122 Million cell updates/sec Pun on:

Tabular output not generated

>US-08-844-215-5 (1-124) from US08844.15.pep 926 1 EVQLLESGGGVVQPGPSURL Description: Perfect Score:

IKGPYYLENWGQGTLVTVSS 124 Sequence.

PAM 150 Gap 11 Scoring table:

111726 segs, 13889129 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq30 1 part1 2 part2 1 part1 4 part4 5 part5 6 part5 7 part7 8:part4 8 part4 10 part10 11 part11 12 part12 13 part13 14:part14 15:part15 16:part21 12 part17 18 part13 19 part12 20 part20 21 part21 22 part22 23 part23

Mean 30.371; Variance 159.298; scale 0.191 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMAPIES

Pesult No.	Score	Query Match	å Query Match Length DR	E C	10	Description	Pred. No.
	706	76.2	192	7	R38161	Sequence of the heavy	7.590-46
7	695	75.1	119	18	R95216	Human foetal immunogi	5.74e-45
٣	692	74.7	123	23	W15534	Anti-TGF beta-1 scFv	9.96e-45
4	691	74.6	123	64	W13531	Anti-melanoma antibod	1 200-44
Ŋ	069	74.5	111	C)	R12275	Anti-human RhD HAM-B	1.440-44
9	685	74.0	115	4	R22571	Heavy chain VH3.5 fro	3.60c-44
7	684	73.9	120	17	R52064	Heavy chain variable	4.330-44
80	683	73.8	123	53	W15535	Anti-TGF beta-1 scFv	5 200-44
6	683	73.8	141	5.	W01522	Monoclosal antibody P	5.200-44
10	683		141	ć.	W24984	Monoclonal antibody P	5.200-44
11	681	73.5	506	7	P12134	ORF 3 of 4B9 human MA	7.51e-44
12	677	73.1	143	σ	R54047	Sequence of the VH re	1.57e-43
13	674	72.8		σ	R50315	Humanised heav; chair	2.72e-43
14	673	72.7	125	6	R54784	SpA-reactive IgM heav	3.26e-43
15	672	72.6	C1	6	250312	Humanised heavy chain	3.92e-43
16	671	72.5	115	33	W15522	Anti-TGF beta-2 scFv	4 710-43
17	670	72.4	122	σ	R50311	Humanised heavy chain	5 668-43
18	699	72.2	126	u)	R28746	Heavy chain variable	6.80e-43
19	999	72.1	140	23	W13524	Anti-melanoma antibod	8.17e-43
20	564	71.7	117	C1	R66323	Human immunoglobulin	1.70c-42

.70e-4	100-4	.46e-4	5e-4	550-4	0000	7.396-42	.07e-4	07e-4	.28e-4	.546-4	.54e-4	.20e-4	.20e-4	0e-4	.67e-4	52e-4	160-4	16e-4	390.4	.39e-4	.39e-4	.67e-4	676-4	70-4
.TGF beta.	heavy	human RhD RE	ti-interleukis-1-a	-963 anti	-109/112-61/h1-12	an anti-HBs	ve IgM	A-reactive	i-melanoma	Human immunoglobulin	#3 for a	antibody C	-human IL-4	-human 1L-4	i-TGF beta-2	MH4H7 MAb heavy chain	Consensus humanised m	Xenograft antibody HA	TNF bind	chain vari	Heavy chain #1 for an	Anti-HIV Fab rev9(VH3	Human anti-HIV Fab am	Anti-melanoma antibod
(-)	15.	227	539	90	633	R42066	478	478	353	632	29.5	Q)	940	ij.	552	153	140	520	500	206	392	806	873	(م. اک
33	٢	c 1	رم. 14	C.1	Ç,	αx	σ	σι	23	Ci	C)	C1	14	14	23	w,	Ç,	6.1	٠.	17	20	12	22	.Y.
(1	CI	r-1	4	₹.	Ci	459	C4	CA	C1	r = 1	<b>+</b> 4	C 1	4	121	-	~₹	CI	₹.	٠.	-1	<del></del> 4	123	CI	*** **** ***
71.7	٦	٦.		- 1	- 1	70.8		0	0	·	c)	·	Ċ.	70.0	6	σ,		σ,	o.	o,	σ.	σ\	σi	0.69
799	664	662	299	5.50	وون	929	654	654	653	652	C039	648	648	548	644	642	547	641	0.40	640	640	639	639	639
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                                                                                                                                                                          A novel recombinant DNA molecule which encodes a single chain fusion protein or antibody comprising the FV region of both the light and heavy chains of an antibody (Ab) fused together, and an effector molecule, where the fusion protein or Ab has the binding specificity of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production of such fusion proteins or antibodies. The fusion proteins can be used in compositions as an immunotoxin to inhibit tumour cell growth. The single chain antibody can be used to detect the presence or
human variable region heavy chains have a cysteine at this posn. i.e. Kabat posn. 59.
Sequence 192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       absence of cells bearing a Lewis(Y) carbohydrate antigen in a patient. The antibodies are also useful as multiple targetting moieties, providing at least 2 kinds of biological activity. They can also be used in diagnostic assays and for the imaging of tumours when attached to a radiolabel and for the pathological diagnosis of tumours. Humanised antibodies are less immunogenic than the mouse MAbs B1, B3 and B5, making them more suitable for long term
                                                                                                                       1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNOYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single chain fusion proteins and antibodies - useful to diagnose and treat cancer, specifically bind Lewis(Y) related carbohydrate
                                                                                                         20 qvqlvesgggvvqpgrslrlscaasgftfssygmhwvrqapgkgldwvavisydgsneyc 79
                                                                                3; Caps
                                                                                                                                                                                                                                                                                                                                                Antibody; fusion protein; single chain; inhibition; tumour; diagnosis; detection; imaging; immunotoxin; targetting; assay; immunoassay; Lewis(Y) carbohydrate antigen.
                                                     Score 706; DB 7; Length 192; Pred. No. 7.59e-46;
                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                     Human foetal immunoglobulin 5681 CL variable heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-OCT-1994; US-33159/.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                14; Mismatches
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L, Pastan I, Willingham M;
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R95216 standard; protein; 119 AA.
                                                        76.28;
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                                                                   77.0%;
                                                                     Best_Local Similarity 77.0%;
Matches 97; Conservative
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Padlan EA, Pai L, Pasta
WPI; 96-251462/25.
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28-OCT-1994; US-331397.
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Gaps

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Score 695; DB 18; Length 119; Fred. No. 5.74e·45; 14; Mismatches 8; Indels 5

Ouery March 75.1%; Best Local Similarity 78.2%; Matches 97; Conservative

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61 adskkyiftisidaskotlylqmoslraedtavyycaktqeyrqqqqssq odowqkqftv 119
                                                                                                                                                                                      61 adsvkgrftisrdnskntlylqmnslraedtavyycarr----sart-yyidywqqqtlv 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transforming growth factor beta lor 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e q for control of fibrosis, immune and inflammatory disease.

Claim 16: Fig la(i): 1849b; English.

This polypeptide sequence comprises the VH domain of human scFV antibody lBZ (also known as TA3), which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (TG0380) isolated from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see WiS522 40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of EGE beta, such as (i) promotion of fibrosis (in dermal, coular or keloid scarring, lung fibrosis, arterial injury, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 1; Gaps
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l gvelvesggggvygpgrslriscaasgftfssyambwyrgapgkglewyavisydgspkyy 60
                                                              1 EVQLLESGGGVVQPGRSLPLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-NoV-1997 (first entry)
Anti-TGF beta-1 scFv antibody 1-B2 VH domain.
Transforming growth factor beta-1; TGF-beta-1; human;
antibody engineering; scFv. phage display; lung fibrosis;
artterial injury; proliferative retinopathy; retinal detachment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scleroderma; vascular didease; cataract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease; macrophage pathogen infection; therapy.
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n JE, Vaughan TJ, Williams AJ;
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Pred. No. 9.96e-45;
15; Mismatches 14;
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Bacon L, Green JA, Jackson RH, John:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W15534 standard; Protein; 123 AA.
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06-OCT-1995; GB-020486.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphoryres (PBLS) of a cancer patient; (b) screening for anti-tumour antibodies in the phage library in a binding assay with cultured tumour cells of the same type as the patient's tumour; (c) removing extraneous antibodies by absorption against normal human cells; (d) cloning the phage selected in step (b) and (c); (e) assaying the specificity of the cloned phage by incubating the phage with at least two types of cultured normal cells; and (f) further besting the specificity of cloned phage that do not bind to either cell line of cultured from more than one other tumour that is not the patient's tumour. The present sequence represents a human heavy can be an antibody, from an scrv antibody fusion phage library, produced by a method as described above The antibody fusion phage library, produced by a method as described above The antibody fusion phage library, produced by antigens for studying tumourigenesis or for use as anti-cancer vaccines. The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MADS). Since the antibodies are isolated
61 adsvkgrftisrdnskkntlylqmnslraedtavyycargfpygg-nsdygmdvwdhgtq 119
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Prod. No. 1.200-44;
17; Mismatches 12, indels 2; Gaps
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                                                                                                                                                         Wi3531;
28-607-1997 (first entry)
Anti-melanoma antibody heavy chain clone V575.
Human; monoclonal antitumour antibody; peripheral blood lymphocyte,
cancer; tumourigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodm. of human monoclonal anti-tumour antibodies - by screening a fusion phage library produced using peripheral blood lymphosytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from fusion phage libraries, their affinity and specificity for a tumour cell line can be improved by genetic manipulations.
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                            W13531 standard; protein; 123 AA.
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Best Local Similarity 75 0%;
Matches 93; Conservative
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28-JUN-1996; IB1032.
30-JUN-1995; US-497647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from a cancer patient
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Cai X, Garen A;
WPI: 97-109061/10.
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Disclosure, Fig 14, 732p, English.

The DNA sequence of eleven monoclonal antibodies are represented in 0.1914-5-7. Synthetic genes, for both heavy and light chains may be created by combining selected CDF 1, 2, and 3 regions, which may be selected from different antibody mols. having varied binding specificity. The chimacric anti-Rhb antibodies can be used for diagnosis and therapy, and are capable of providing blood-typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ggvvqpgrslrlscaasgftfssygmhwvrqapgkglewvaviwydgsnkyyadsvkqrf 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 74.5%; Score 690; DB 2; Length 111;
Best Local Similarity 79.5%; Pred. No. 1.44e-44;
Matches 89; Conservative 13; Mismatches 7; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 GGVVQPGPPSLPLSCAASGPTFSAYGMHWVPQAPGKGLEWVAGIWFDGSNQYYSDSVKGPF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ed; bacteriophage, gene ili, filamentous; phagemid, capsid, cout, plius; g3p, binding, adsorption; gene VIII, diverse repertoire, specific binding pairs, replicable genetic display package, human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEDT-) MED RES COUNCIL.
McCafferty J. Pupe AR. Johnson KS. Hoogenboom HRJ. Griffiths AD.
Jackson PH. Holliger KP. Marks JD. Clackson TP. Chiswell DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 TVSPENSRNILFLOMNSLRPELTAVYYCAIEV-LFGSIKGRYY-LENWGQGI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding complementary determining regions - of human anti-rhesus D antibodies, useful in prodn. of monoclonal antibodies and for passive immunisation
                                                                 15-Aug-1991 (first entry)
Anti-human RhD HAM-R MB (VH chain)
Monoclonal antibody; thesus D; blood-typing; CPR;
haemolytic disease of the newborn; HDN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heavy chain VH3.5 from BSA binding scFv fragment.
                                                                                                                                                                                         Location/Qualifiers
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R22571 standard; Protein; 115 AA.
.T 5
R12275 standard; Protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (BLOG-) CENT BLOOD LAB AUTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CAMB-) CAMBRIDGE ANTIRODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                      91 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-00T-1990; GB-022845.
12-NOV-1990; GB-024503.
06-MAR-1991; GB-004744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-1991; GB-010549.
                                                                                                                                                                                                                                                                                                                                                                                                                    GR-025590
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10-JUE-1990; GB-015198.
                                                                                                                                                                                                               23..27
                                                                                                                                                                                                                                                          42..58
                                                                                                                                                                                                                                                                                                                                                                           30-MAY-1991.
13-NOV-1990; E01964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 91-178104/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hughes - Jones N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB: 011957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
W09201047-A.
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Jackson PH, H
                                                                                                                                                                                                                                                                                CERT
                                                                                                                                                                                                            Region
/label- CDR1
                                                                                                                                                                                                                                                                                                                            /label= CDR3
WO9107492-A.
                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-1989;
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JAN-1992
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Cer was used too prepare a human scrot ineray chains from white

blood cells from an unimumised donor. Heavy chains from IgG and

blood cells from an unimumised donor. Heavy chains from IgG and

control of the control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
74.0%; Score 685; DB 4; Length 115;
Best Local Similarity 78.0%; Pred. No. 3.60e-44;
Matches 92; Conservative 14; Mismatches 9; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 adsvkgrftisrdnskntlylgmnslraedtavyycaktg-yssgwg-yf-dywgggt 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method of resurfacing of rodent antibodies to produce humanised antibody forms - for producing non-human antibodies with improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-007-1996 (first entry)
Heavy chain variable region of human G36005 antibody.
antibody; humanised; murine; human; heavy chain: light; variable; framework region; complementarity determining region; reshaping; modelling; surface residue; modify.
                                                                producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pedersen JT, Rees AP, Roguska MA, Searle SMJ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= complementarity_determining_region_1
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                                                                                                                                                                                                 Table 11; Page 152; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R52064 standard; Protein; 120 AA.
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Winter GP, Bonnert TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-1993; 307051.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 AA;
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                                                                                                                                                               display package.
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therapeutic efficiency by presenting human surface on V-region

Example 1; Fig 4B; 230pp; English. Ab) or Iragment by resurfacing in

Modification of a rodent antibody (Ab) or Iragment by resurfacing in

corder to produce a humanised rodent Ab can be determined by calculating

corder to produce a humanised rodent Ab can be determined by calculating

corder to produce a humanised rodent Ab can be determined by calculating

corder to produce a humanised rodent Ab can be determined by calculating

corder to produce a humanised rodent Ab can be determined to the invention. Unsee humanisation experiments

corder to produce to the invention, three humanisation experiments

corder to resurfacing approach

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corder to treat in order to test

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of librosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVOLLESGĞĞUVÇPGRELRLECAASGFTFSAYGMHWVPQAPGRGT.FWVAGTWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.9%; Score 684: DB 17; Length 120; 77.2%; Pred. No. 4.33e-44; vative 14; Mismatches 11; Indels 3: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune and inflammatory disease
claim 16; Fig 1a(i1); 184pp; English.

This polypeptide comprises the VH down of human serv antibody 31G9, which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (T60381) isolated from a large beta-1. It is encoded by a gene (T60381) isolated from a large shingle chair for intary. The antibuse-linding decaping of human antibodies (see W1522-44), to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (1) promotion to counter the adverse effects of TGF beta, such as (1) promotion or inhors, in the following attential injury, prohiferative rethnopathy, retinal detachment, adult resplitting distress syndrome. Hier rithousis, post
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adult respiratory distress syndrome; liver cirrhosis; post myocardial infarction; post-angioplasty restenosis; scleroderma; vascular didease; cataract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthitis; macrophage deficiency disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-TGF beta-1 scFv antibody 31G9 VH domain.

Transforming growth factor beta-1; TGF-beta-1; human;
antibody engineering; scFv; phage display; lung fibrosis;
arterial injury; proliferative retinopathy; retinal detachment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CAMB.) CAMBRIDGE ANTIBODY TECHNOLOGYS (CAMB.) CAMBRIDGE ANTIBODY TECHNOLOGYS (S. POPE AR: PROMEST PR. Thompson JE, Vaudhan TJ, Williams AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        macrophage pathogen infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 8
W15535 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 77.2%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-ОСТ-1996; 020920.
19-JAN-1996; GB-001081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-1995; GB-020485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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61 adsvkgrftisrdnskntlylqmnslraedtavyycartgeysgydtsg-velwgggttv 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLLESGGGVVQPGRSLFLSCAASGFIFSAYGMHWVRQAPGKGLEWVASIWFDGSNQYY 60
               Agoular discretes, catract, glaucoma, or esp neural scarring and glomerulonephritis, also (for claimed) ustoupcrisis), or (ii) immune and inflammatory diseases (e.g. rheumatorid arthritis, macrophage deficiency diseases or macrophage pathry no fercion) Nucleic acids encoding human antibody VH and VL can be used for prodn. of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM)
                                                                                                                                                                                                                                                                                                                                                                            Indels 1, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03.4MR-1997 (first entry)
Monoclonal antibody PE1-1 heavy chain variable region.
Monoclonal antibody; diagnosis; treatment; infection; hepatitis B;
xenogeneic hybridoma, SFAZ 4; FE1-1, SM1-1, SM1-1, M3-4, 103-3,
IgGl class, heavy chain; light chain; variable region.
myocardial infarction, post-angioplasty restenosis, scleroderma,
                                                                                                                                                                                                                                                                                                                 Score 683, DB 23; Length 123;
Pred. No. 5.20e-44;
14; Mismatches 15, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- complementarity_determining_region_1
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                                                                                                                                                                                                                               and low IC50s for neutralisation.
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Region 118..129
                                                                                                                                                                                                                                                                                                                 Match 73.8%;
Local Similarity 75.8%;
les 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- V_H(III)_region
Region 20..49
/label- framework_region_1
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15.JUN-1990; US-538796.
27.MAR-1991; US-676036.
21.AFR-1992; US-877426.
14.JUN-1994; US-259372.
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31-CCT-1986; US-925196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T46128
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/label= CDR2
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                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                        Query Match
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08-DEC-1997 (first entry)
Monoclonal antibody Bell 1 Wh region.
Heavy chain: light chain; variable region, human, monoclonal antibody:
Heavy chain: light chain; variable region, human, mouse; fusion, xenogeneic;
Immunisation; hepatitis B virus; HBV, vaccine; mouse; fusion, xenogeneic;
peripheral blood hymphocyte; surface antigen; cell culture; ion exchange;
chromatography; size separation; primer; PCR; polymerase chain reaction;
applification, hybridema, infection, immunosuppression; hepatitis;
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                        The state of the s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SDSVKGRFTVSRDNSRNTLFLOMNSLRPEDTAVYYCATFVL, FGSIKGRYYLENWGQGTL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 grglvosgggvvgpgrslrlscaasgftfsrygmhwrrqapgkglowravisydgspkwy 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 683, DB 19, Length 141;
Prod No. 5 20e-44;
10; Mismatches 14; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVOLLESGGGVVQPGPSLPLSCAASGFTFSAYGMHWVPQAPGKGLEWVAGIWFDGSNQYY AO
Human monoclonal antibodies specific for hepatitis B surface antiqen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of hepatitis R - with human monoclonal antibody Example 8, Column 15-18, 25pp, English.
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Domain 69..85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tarity determining region 2"
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Best Local Similarity 77 6%,
Matches 97, Conservative
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"mature protein"
20..117
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15-JUN-1990; US-538796.
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14-JUN-1994; US-259372.
06-JUN-1995; US-468671.
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Domain 50..54
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N-PSDB; T85838.
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This is the amino acid sequence of the heavy chain variable (Vh) region from the human monoclonal antibody (MAb) PEI-1. The MAb was generated by immunising humans with a hepatitis B virus (HBV) vaccine, isolating by immunishing humans with a hepatitis B virus (HBV) vaccine, isolating be peripheral blood lymphocytes (PEL) and fusing them with a mouse/human compared cell line SPAZ-4. 5 cell lines were isolated: PEI-1, ZMI-1, MD3-4 and LO3-3. The cell lines were then tested for production of a nati-hepatitis B virus surface antigen antibody by ELISA. The MAbs conformatography, size separation on Sephacryl S300 gel and ion exchange chromatography on Q-sepharose. The heavy and light chains of the MAbs choranted and used to amplify cDNA synthesised from RNA purified from generated and used to amplify cDNA synthesised from RNA purified from generated and amino acid sequences of the heavy and light chains contain a mimo acid) from MAbs PEI-1, ZMI-1, ZMI-2 and MD3-4 are contain a mimosuppressed patients or patients with chronic active horatics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDSVKGRFTVSPDNSRNTLFLQMNSLRPEDTAVYYCATEVL-FGSIKGRYYLENWGUGTL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 qvqlvesgggvvqpgrslrlscaasgftfsrygmhwvrqapgkglewvavisydgsnkwy 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVOLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is derived from the nucleotide sequence encoding the heavy chain variable region. The "x" residues represent nonsense codons. The coding sequence has been translated in all 3 reading frames (see also R12132 and R12133).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligomeric immunoqlobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of 19G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (first entry)
ORF 3 of 4B9 human MAb heavy chain variable region clone.
immunoglobulin G; heavy chain; variable region; dupilcation.
                                                                                                                                                                                                                                                                                                                                                                               Score 683; DB 23; Length 141;
Pred. No. 5.20e-44;
10; Mismatches 14; Indels 4
                                                                                                                                                                                                                                                                                                                             hepatitis, especially liver transplant patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "last 3 residues of leader and variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region; the rest of leader is translated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        passive immunity; group B streptococci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R12134 standard; Protein; 506 AA.
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Shuford WW, Harris LJ, Raff HV;
                                                                                                                                                                                                                                                                                                                                                                                   y Match
Local Similarity 77.6%;
nes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244..369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAY-1991.
06-NOV-1990; 006426.
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Gaps

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Score 681; DB 2; Length 506; Prod. No. 7.51e-44; 14; Mismatches 13; Indels

Local Similarity 76 68: es: 95; Conserved

Query Match

Matches:

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Example, Page 35, 53pp, Bonglish.

Example, Page 35, 53pp, Bonglish.

Human volunteers were immunised with hepatitis B varcine. MD1-4, ZM1-

Human volunteers were immunised with hepatitis B vaccine. MD1-4, ZM1-

Hymphocytes of individuals immunised with Heptavax (Merck 6 CO).

Jymphocytes of individuals immunised with Heptavax (Merck 6 CO).

Antibodies PEI-1, ZM1-1, MZ1-2 and MD3-4 belong to the Idd) clus.

Artibodies PEI-1, ZM1-1, MZ1-2 and MD3-4 belong to the Idd) clus.

Artical Innes producing PEI-1, ZM1-1 and ZM1-2 were deposited as ArcK H9234, 9191 and 9192 respectively. The cell lines all behave as typical (mouse x human) x human hybridomas and produce their respective Abs in concs. Iddiiguague to 25 ma/1 in standard suspension culture. The heavy variable (VH) and light variable (LH) channel of Abs Experies and MD3-4 were isolated and concerned.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 gyglyesgggyydpgrslrlscaasaftfsrygmhwyrgapykglewyavisydgsnkwy 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 qvqlvesgggvvqpgislrlscaasgftfrsygmhwyrqapgkglewvavissdqsvdyy 306
                                                                                                                       307 adsvkgrftisrdnsrdmlyvqmnsiraedtavyycakekosggr scysfdywqqqtlv 364
                                                                                                                                                 Gaps
                                                          1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVPQAPGKG1FWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequenced Total RNA was extracted from 10(7) hybridoma cells of each cell line. Ss DNA was synthesised using AMV-reverse transcriptase and oligo-dT as primer. PCRs were performed and amplified DNA was size selected. Ss DNA for sequencing was isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatitis B virus surface antigen. monocional antibody; therapy; HBSAG; diagnosis; HBV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibodies active against Hepatitis B surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing was by the dideoxy chain termination method (Sanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of the VH region of monoclonal antibody PE1-1 against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       R54047 standard; Protein; 143 AA.
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ilarity 76.6%;
Conservative
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nes 95; Conser
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Ostberg LG;
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                                                                                                                                                                                                                                                                                                                      121 TVSS 124
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Pelease 2.10 John F. Collins, Riccomputing Fesearch Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:09:05 1998; MasPar time 5.25 Seconds 504.498 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-844-215-4 (1-125) from US08844215.pep 921 Description: Perfect Score:

1 EVQLLESGGGVVQPGRSLPL. ..... IKGRYYLENWQQTLVIVSS 125 Sequence.

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210399 residues Searched.

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 swiss-prot34

Mean 42 149; Variance 77.571; scale 0.543 Statistics. Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

S.	122	111	111	110	102	~	98	13.	-	95	94	94	۲.	92	r:1	68	$\alpha$	m	47	0.1	86	
Pred.	9.640-	7.450	2.51e-10	3.19e-1	1 670-1	0.13	1.51er	9	2.50e-	1.78e·	1.34e-	6.08e-9	1.670-	9.37e-9	4 240-	.37e-	6.48e-8	6.48e-8	ونات		1	4 95p
1	V-III	V-111	V-III	V-III	Tii-A	PRECITE	V-III	V-III	V-III	V-III	V-III	V-III	PPECUP	V-III	V-III	V REGI	V-III	V-III	PPECTE	РРЕСТИ	V REGI	PRECUP
go	CHAIN	CHAIN	CHAIN	CHAIN	NIAHO	CHAIN	CHAIN	CHAIN	CHAIN	CHAIN	CHAIN	CHAIN	CHAIN	CHAIN	CHAIN	CHAIN	CHAIN	CHAIN	CHAIN	THAIN	CHAIN	CHAIN
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an	HV3G_HUMAN	HV3H_HUMAN	HV3K_HUMAN	HV3J_HUMAN	HV3 I_HUMAN	HV3C_HUMAN	HV3E_HUMAN	HV3A_HTMAN	HV3L_HUMAN	HV3U_HUMAN	HV3T_HUMAN	HV3N_HUMAN	HV16_MOUSE	HV3M_HUMAN	HV3F_HUMAN	HV02_CANFA	HV3B_HUMAN	HV3D_HUMAN	HVOS_CAPAL	HV01_PAT	ای،	HASE WOLLSE
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                                                                                                                                                                                                                                                          1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                      3; Gaps
                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (GA).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDAIA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                            Score 679; DB 5, Length 122;
Pred. No. 7.46e.121;
30; Mismatches 12; Indels
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                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID
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SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N.;
HOPPE-SEYLER'S Z. PHYSIOL. CHFM. 364:713-747(1983).
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X-KAT CALLIAGO.

MARQUART M. DEISERHOFER J. . HUBER R., PALM W.:

MARQUART M. DEISERHOFER J. . HUBER R., PALM W.:
                                                                                                                                                                                122 122
122 AA; 13166 MW; D68B085E CPC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (KOL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                              Query Match
Best Local Similarity 64.0%;
Matches 80; Conservative
                                                                                                                                                         IMMUNOGLOBULIN V REGION.
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PIR; A02055; G1HUKL.
PDB; 2FB4; 12-JUL-89.
PDB; 2IG2; 12-JUL-89.
                                                   EUTHERIA; PRIMATES.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLLESGGGVVQFGRSLRLSCAASGFTFKTYGMHWVRQAFGKGLEWVAGISFPGSNOYY 60
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.4%; Pred. No. 3 19m-110;
Matches 83, Conservative 20; Mismatches 18: Indels 4; Gaps
                                                                                                                                                                                                                                                                                            Score 636; DB 5; Length 126;
Pred, No. 2.51e-111;
18; Mismatches 20; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVKUAFGKGLEWVAGISFTGSNOYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT H43J_HUMAN STANDARD, FRT; 121 AA.
H43J_HUMAN STANDARD, FRT; 121 AA.
21-JUL-1986 (REL 01, CREATED)
21-JUL-1986 (REL, 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL, 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (HIL).
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA: MAMMALIA; EUTHERIA; PRIMATES.
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121 AA; 13566 MW; 8E91B7EC CRC32:
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                                                                                                                                                                                                                                                                                                         69.1%; Score 636;
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nes 87; Conservative
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HV31_HUMAN
P01770;
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLLESGGGVVQPGFSLFLSCAASGFTFKTYGMHWVFQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
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EUKARYOTA; METAZOA; CHOPDATA; VEPTEBRATA; TETPAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ö
                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETPAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                 Length 119
                                                                                                                                                                                        DPEREZ., SCHWARZ. J., PEICHEL W., HILSCHMANN N.; HOPPEF.SEYLER'S. Z. PHYSIOL. CHEM. 357:1515-1540(1975).
-!- THIS CHAIN WAS ISOLATED FROM AN IGSI MYELOMA PROTEIN. PIR, A02053, GIHUNI.
HSSP, PO1667. LFGV.
                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                 PYPROLIDONE CAPROXYLIC ACID
                                                                                                                  MEDLINE: 77070269.
PONSTINGL H., HILSCHMANN N.;
HOPPE-SEYLEP'S Z. PHYSIOL CHEM. 357:1571-1604(1976)
                                                                                                                                                                                                                                                                                                                                                                          23; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATTHYSENS G., RABBITTS T.H.;
PROC. NATL. ACAD. SCI. U.S. A. 77.6561-6565(1980)
EMBL, J00236; G553412;
EMBL, M35415; G553422;
EMBL, M36417; H34026.
PIR, A02647; H34026.
IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                 Score 596; DB 5, La
Pred. No. 1.67e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 578; DB 5,
Pred No. 1 51e-98;
                                                                                                                                                                                                                                                                                                         119 119
119 AA; 13242 MW; 5703CA8E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA; 12582 MW; 15A21B2A CRC32;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SECUENCE UPEATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
10-COT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PPECURSOP V-III REGION (VH25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 62.8%;
Local Similarity 77.3%;
Los 75; Conservative
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.8%;
                                                                                                                                                                                                                                                                                                                                                                           81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                    IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                            96
                                                                                EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 81101090
                                                                                                                                                                                       MEDLINE; 77070267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 vtvss 119
                                                                                                                                                                          DISULFIDE BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HV3C_HUMAN
P01764;
                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                           SEQUENCE.
                                                                                                                                                                                                                                                                                            DISULFID
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                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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20 evgllesggglvqpggslrlscaasgfffssyamswvrqapgkqlewvsaisgsggstyy 79

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19; Mismatches 17; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM TYPE. PIR; A02049; M3HUBW.
HSSP, P01772, LEGV.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZGA; CHORDATA; VEPTEBRATA; TETRAPODA: MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKAPYOTA: METAZOA: CHOPDATA; VERTEBRATA; TETPAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 76023781.
MEDLINE; 76023781.
HILSCHWANN N.; HURSCHWANN N.; HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:1337-1342(1975).
PIP: ACCOUNTE OF THE C REGION IS ALSO GIVEN.
HISP: ACCOUNTE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYPPOLIDONE CAPBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 578; DB 5;
Pred No 1 51e-98;
                                                                                     80 gdsvkgrftisrdnskntlylqmnslraedtavyyca 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 122
122 AA: 13472 MW: BFCOD358 GRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 120 120 120 AM; B404C4F1 CRC32;
                                                                                                                      61 ADSVKGPFIVSPDNSPDTVFLQMSSLRLEDTAVYYCA 97
                                                                                                                                                                                                                                                                                                                   21-JUL-1996 (PEL. 01, CREATED)
21-JUL-1996 (PEL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (PEL. 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-III REGION (BRO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                      PPT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V-III REGION (TRO).
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAPPA J D , HOPPER J E ;
IMMUNOCHEMISTRY 13:995-999(1976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE (MYELOMA PROTEIN TRO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P01762;
21-JUL-1986 (PEL. 01, CPENTED)
21-JUL-1986 (PEL. 01, LAST SEQUED)
21-JUL-1986 (PEL. 01, LAST SEQUED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 62.8%;
Local Similarity 65.9%;
es 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                   STANDARD;
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P01766;
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SEQUENCE
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SEQUENCE
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Match 60.8%;
Local Similarity 67.2%;
les 84; Conservative
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Best Local Similarity 63.2%;
Matches 79; Conservative
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                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                  IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A02064; M3HUGL.
HSSP; PU1607; 1FGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 75059123.
WATANARE S , RAPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 vtvst 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HILSCHMANN N.;
                                                                                                                                                                                                                                                               116 vtvss 120
                                                                                                                                                                                                                                                                                      121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                HV3T_HUMAN
P01781;
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SEQUENCE
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61 ADSVKGRFIVSRDNSRDTVFLQMSSLRLEDTAVYYCATEGSPFGSIKGRYYLENWGQGTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l qvqlvqsggglvkpggslrlscvasgfsfrdfymswirztpgkglzwvsylggsgstlyy 60
                                                      1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 6U
Best Local Similarity 56.8%; Pred. No. 1.51e-98;
Matches 71; Conservative 29, Mismatches 22; Indels 3, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sdeb (9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAÎN V-III REGION (DOB).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VEPTERRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 577; DB 5; Length 119;
Pred No 2 50e-98;
22; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MADLINE, 80020921.
STEIMER L.A., GARCIA PARDO A., MARGOLIES M.N.;
BIOCHEMISTRY 18:4068-4080(1979).
                                                                                                                                                                                                                                                                                                                                                                                                      28 28
119 119
119 AA; 12981 MW; 323A4FE1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-501-986 (RFL 01, CREATED)
21-501-1986 (REL 01, LAST SEQUENCE UPDATE)
01-NOV-1995 (PEL 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                             21-JUL-1985 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                          119 AA.
                                                                                                                                                                                                                                                                                                                         PUTNAM F.W., LIU Y.-S.V., LOW T L K; J. BIOL. CHEM. 254:2865-2874(1979) PIR; A02056; Alhubr.
                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULIN V REGION; GLYCOPPOTRIN
                                                                                                                                                                                                                                               IG HEAVY CHAIN V-III REGION (BUR).
                                                                                                                                                                                                                                                                                                      SEQUENCE (MYELOMA PROTEIN BUR).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 62.6%;
Local Similarity 63.7%;
les 79, Conservative
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                                                                                                                                                                                             STANDARD.
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58
                                                                                                                                                                                                                                                                                  EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                   MEDLINE; 79151016.
                                                                                                                            118 vtvss 122
                                                                                                                                                 121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 vtvs 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VTVS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HV3U_HUMAN
                                                                                                                                                                                            HV3L_HUMAN
P01773;
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SCOUENCE.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                     21, Mismatches 20, Indels 5: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           1 evqlvesggdlvqpqrslrlscaasqfnfheynmhwlrqgpgkqpewvstitwnqqsvly 60\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLLESGGGVVQFGRSLRLSCAASGFTFKTYSMHWVPTAFFKTKTFFWATISFFGSNOYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Caps
CRYSTALLIZATION.
MEDLINE, ROD20920.
STEINER L.A., LOPES A.D.;
BIOCHEMISTRY 18:4054-4067(1979).
-!-THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE HINGE REGION.
-THES GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE HINGE REGION.
PIRE ARE NO LIGHT-HEAVY OF INTER-HEAVY CHAIN DISULFIDE HONDS.
PIR; A02065; GIHUDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (JUN-1975) TO THE PIR DATA BANK.
-!- THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOHULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WATNUARE S, RAPNIKOL H II, HORN J., BERTRAM J., HILSCHMANN N.:
HOPPE-SEYLER'S Z, PHYSIOL, CHEM. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V-111 RESTON (GAL).

IGNO SAPIENS (HUMAIN).

EUKARYOTA: MEIAZOA, CHOKDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 560; DB 5; Length 116;
Pred, No. 1.34e-94;
18; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                           Length 120;
                                                                                                                                                                                                                                                                                                         Score 564; DB 5; Pred, No. 1.78e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 116
116 AA; 12730 MW; F112826G CPC32;
                                                                                                                                                                                                                                NON_TER 120 120
SEQUENCE 120 AA, 13440 MW. 100CHSOF CFC72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISION TO THE COMPOSITION OF 28-33.
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                                                                                                                                                                                                                                                                                                          61 adsvngrftisrndskntlylqmnglqazvsaiyycardagpy--vsptff-ahwgqgtl 117
                                                                                                                                                                                                                                                                                                                              61 ADSVKGPFIVSPNSPDTVFLQMSSLRLEDTAVYYCATEGSPFGSIKGPYYLENWGGGTL 120
                                                                                                                                                                                                                                                                    2 vqllesgqglvqpgqslrlscaasgftfsasamswvrqapgkqlewva-wkyengndkhy 60
                                                                                                                                                                                                                                                                                       2 VQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFD-GSNQYY 60
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE, 81234548.
BOTHWELL A.L.M., PASKIND M , PETH M , IMANISHI-KAPI T , PAJEWSKY K
                                                                                                                                                                                                                                                Ľ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V PEGION (MOPC 21)
                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA: CHORDATA: VEFTEBFATA: TETFAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUS MUSCULUS (MOUSE).
EUKAPYOTA, METAZOA, CHOPDATA, VERTEBPATA, TETFAPOGA, MAMMALIA,
                                                                                                                               PROC NATE ACAD. SCI. U.S.A 71-4032-4035(1974).
                                                                                                                                                                                                                           Length 119;
                                                                                                                                                                                                                                               29; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       P01783,
21-JUL-1986 (PEL 01, CREATED)
21-JUL-1986 (REL 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PPECURSOR V REGION (MOPC 21) (FRAGMENT).
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DN -> ND (IN REF. 2)
                                                                                                                                                                                                                          Score 557; DB 5;
Pred. No. 6.08e-94;
                                                                                                                                                                                             NON_TER 119 119
SEQUENCE 119 AA; 12858 MW; 1CE0116C CRC32;
                            21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III PEGION (LAY).
119 AA.
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NATURE 265:299-304(1977).
EMBL; J00522; G195055; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 PPT;
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMUNOGLOBULIN V REGION: SIGNAL
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                   21-JUL-1986 (REL. 01, CREATED)
                                                                                                                                                                                                                          Query Match
Best Local Similarity 59.0%;
Matches 72; Conservative
                                                                                                                                                                      HSSP; P01772; 11GM.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
 STANDARD;
                                                                                                          MEDLINE; 75046755.
CAPRA J.D., KEHOE J.M.;
PROC NATL ACAD. SCI. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JEIL 24 625-637 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR: A02066; GIMS21.
HSSP; P01607; 1FGV.
                                                                                                                                                                PIR; A02058; M3HULY.
                                                                                EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 17-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; RODENTIA
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120
120
38
136
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 HV3N_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DISULFID
                                                                                                    SEQUENCE.
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CONFLICT
CONFLICT
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60 yadsvagifiisindsknilyllmsiqarbialyycardagpy--ysptfi-ahyaqqt 116
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                                                                                                                                                                                                                                                            77 adtvkgrftisrdnpkntlflgmtslrsedtamyycarwgn-y-py---yamdywgggts 131
                                                                                                                                                                                                                                                                                     61 ADSVKGRFIVSRDNSRDIVFLQMSSI.RLEDTAVYYCATEGSPRGSTKGRYYLENWGQGTL 120
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                                                                                                                               Gaps
                                                                                                                                                                        17 dvglvesggglvqpggsrklscaasgftfssfgmhwvrqapekglewvayissgsstlhy 76
                                                                                                                                                                                                               1 EVOLLESGGGVVQPGRSLRLSCAASGFIFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
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21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
TG HEAVY CHAIN V-III REGION (BUT).
HOMO SAPIENS (HUMAN).
EUKARYGTA, RETAGA, CHOFFATA, VEFTERRATA; TETRAFODA, MAMMALIA, EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAPPA J.D., KEHOR J M ;
PROC. NATL ACAD SCI. U S.A. 71:4032-4036(1974)
-!- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
                                                                        Score 555; DB 5; Length 136;
Pred No. 1:67e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 547, DB 5, Length 119;
prod No 9,378-92;
28; Mismatches 17; Indels
                                                                                                                               20; Mismatches 18; Indels
115 115 W -> H (IN REF. 2).
120 120 Y -> W (IN REF. 2).
136 AA, 15071 MW; 24BFDEBB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA; 12953 MW; 2A5697D2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1996 (PEL 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
12-JUL-1986 (REL. 01, LAST SAUGATION UPDATE)
1G HEAVY CHAIN V-III PEGIÓN (PÓM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AA
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P01767;
21-JUL-1986 (PEL. 01, CPEATED)
                                                                           Loral Similarity 65.68.
es 82; Consonner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
Decal Similarity 59,34,
es 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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HSSP; P01772; 1FGV.
IMMUNOSLOBULIN V PEGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV3M_HUMAN
P01774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
SEQUENCE
CONFLICT
CONFLICT
SEQUENCE
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Query Match

59.1%; Score 544; DB 5; Length 115;
Best Local Similarity 69.7%; Pred. No. 4.24e-91;
Matches 69; Conservative 17; Mismatches 12; Indels 1; Gaps
[1]
MEDLINE: 78137069.
MEDLINE: 78137069.
TORANO A., PUTNAM F.W.;
PROC. NATL. ACAD. SCI U S.A. 75.966-969(1978).
-!- THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C REGION OF THIS NYELOMA PROTEIN IS ALSO GIVEN.
MYELOMA PROTEIN IS ALSO GIVEN.
HASP: POLTZ: IFGV.
IMMUNGLOBULIN V REGION.
NON_TER 115 115
SEQUENCE 115 AA; 12379 MW; 90803472 CPG32;
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Search completed: Tue Feb 24 07:09:20 1998 Job time : 15 secs.

US-08-844-215-5.rag

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Matches
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*80 adsvkgrftisrdnskntlflqmhslraadtgvyycakdqlyfgsqspghy---wvqgtl 136
                                       61 pdtvtgrftisrdnskntlylqmnslraedtavyycasliyyg-ydg-yamdywgqgtlv 118
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SpA domain D; Ig binding region; IgM: E-cell superantigen; sAg;
superantigen, heavy chain variable region; VH3 restricted antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB, 044640.

New engineered antibodies and fusion proteins for preventing plasmodium infection - contg. murine antibody CBR sequences, an corresp. nucleic acid, vectors and transformed cells claim 14; Fig 9; 98pp; English.

Example 4 describes the prodn. of a high affinity humanised antibody. At amino acid position 49; the Ser of the humanised heavy chain Pfhizhc23 was changed to Ala, which is the amino acid found at this position in the native murine NSF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 674; DB 9; Length 122; Pred, No. 2.72e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised heavy chain variable region Pfhz1c2-6. Monoclonal antibody. Plasmodium falciparum; CDR; complementarity determining region; fusion protein; murine, variable, light; heavy, chain, malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosenberg M;
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Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 WAR-1994.

08-SEP-1993: U08435.

09-SEP-1992: US-941654.

(SMIK) SMITHKLINE BEECHAM COPP.

(USNA) US SEC OF ARMY.

(USNA) US SEC OF NAVY.

(DATOGROVIT Y, HOLIMAN S, HULLE M SAdoff JC, Sylvester DR, Gross MPP: 94-101115/12.
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                                                                                                                                                                                                                                                                                                                                        R50315 standard; Protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.8%;
Best Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                        R50315;
05-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93; Conservative
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29-OCT-1993; U10555.
30-OCT-1992; US-9699
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                                                                                                                                     137 vtvt 140
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61 adsvkgrftisrdnslntlylqmnslraedtavyyctkqqvlyyg-sgsyhwfdpwgqqt 119
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Silverman GJ;
WPI: 94-16/1207/20.

WPI: 94-16/1207/20.

Stimulating prodn. of variable region gene family restricted antibodies - through B-cell super-antigen vaccination Disclosure: page 66; 130pp: English
B-cell superantigen (849) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The SAG is used to enhance production of VH; sepecially VH3, restricted Abs. During attempts to identify sAgs, as sequences (R54784-801) of H chains from Ig reactive with mod-SpA, and as and DNA sequences (F74801; GA4402-56) of VH regions of SpA binders obtained from combinatorial libraries were determined. IgM protein 18/2 derives from the germline configuration of VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 evgllesggglvqpggslrlscaasgftfssyamswvrqapgkglewvsaisgsggstyy 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Match 72.7%; Score 673; DB 9; Length 125;
Local Similarity 73.8%; Pred. No. 3.26e-43;
Les 93; Conservative 17; Mismatches 13; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised heavy chain variable region Pfhzhc2-3. Amonoclonal antibody: Plasmodium faloiparum; CDP; complementarity determining region, fusion protein; murine, variable; light; heavy; chain; malaria
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Gross MS;
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R50312 standard; Protein; 122 AA.
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N-PSDB; 044826.
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09-SEP-1992; US-941654
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Pelease 2 1D John F Collins, Biocomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:04:38 1498; MaxPar time 9.44 Seconds 383.249 Million cell updates/sec Run on

Tabular output not generated.

>US-08-844-215-4 (1-125) from US08844215.pep 921 1 EVQLLESGGGVVQPGPSLPL

Title: Description: Perfect Score: Sequence:

....IKGPYYLENWGQGTLVTVSS 125

Scoring table:

PAM 150 Gap 11

95051 seqs, 30469580 residues Searched.

Minimum Match 0% Listing first 45 summaries Post-processing:

pir53 Database:

Isanil 2:ann2 3:ann3 4:ann4 5:unann1 5:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unann11 16:unann12 17:unann

Mean 41.619; Variance 120 293; scale 0 346 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUFFMARIES					
Result No.	Score	Query	Length	DB	ID	Desc	Description	uc		Pred. No.
				-					1	
н	701	76 1	121	7	519666	F	Y. Fed	chain	V reg	2.396-79
7	989	74.5	151	۲~	A60943	Iq	heavy	chain	precu	3.22e-77
m	584	74.3	122	7	S31117	H	heavy	chain	- hum	6.18e-77
4	683	74.2	ri	C1	M3HDAM	H	heavy	chain	V-III	8.57e-77
'n	680	73.8	12	7	E36005	11	heavy	chain	v red	2.28e-76
Ø	619	73.7	122	C1	M3HUGA	Ιd	heavy	chain	V-III	3.16e-76
7	677	73.5	120	7	536278	14	heavy	chain	V req	6.07e-76
60	672		12	7	S48797	Ig	heavy	chain	v red	3.10e-75
6	670	72.7	11	7	S31116	Ιď	heavy	chain	- hum	5.96e-75
10	670	72.7	12	7	G36005	H	heavy	chain	V red	5.96e-75
11	670	72.7	13	7	531574	p.	heavy	-	V req	5.966-75
12	664	72.1	C1	7	538493	57	heavy		hun.	4.21e-74
13	663		13	۲-	A49028	ы	hear.;	chain	III-A	5.83c-74
14	662	71.9	13	7	S31603	Ιď	heavy	chain	V req	8.08e-74
15	661	71.8	12	7	S31112	EH	heavy	chain	- hum	1.12e-73
16	661	71.8	13	^	S31510	Ιď	heavy	chain	- hum	1.12e-73
17	658	71.4	11	7	3745	Ιď	mu chain	,	human	2.97e-73
18	650	70.6	11	7	F36005	Ιđ	heavy	chain	v red	4.02e-72
19	650	70.6	12	٢	819818	14	hear	n:equ	A red	4 020-72
50	650	70 6	u c c	r	35555	+1	hearry	chain	v reg	4.025.72

A60943 #type complete Ig heavy chain precursor V region (clone HN.14) - human

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RESULT ENTEY TITLE

hain hain hain hain hain hain hain hain	19 Neavy chain v red 5.296-7 19 heavy chain v-III 7326-7 19 heavy chain v reg 7.326-7 19 heavy chain v reg 7.326-7 19 heavy chain v reg 7.326-7 19 heavy chain v reg 1.016-6 19 heavy chain - hum 1.946-6	on (VH3DCH4) - human viens #common_name man _revision 22-Jan-1993 #text_change .m, H.F.; Bonnert, T.F., McCafferty, J.; nter, G. on. Human antibodies from V-gene on phage.	obulin V region; immunoglobulin homology oglobulin homology *label IMM ar-weight 13296 #checksum 9195	701. DB 7; Length 121; No. 2.39e-79; Mismatches 10; Indels 4; Gaps 3; fssygmhwyrgapdyglewyavisydgsnkyy 60; :1[11111111111111111111111111111111111
\$05227 \$21112 \$20782 \$20782 \$44111 \$344111 \$34114 \$31114 \$31167 \$31107 \$31107 \$31107 \$31107 \$31107	3527 6991 1011 4639 3165 3167 3849 1HTH	pe comp V regiono sap cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence cquence c cquence c cquence cquence cquence c cq cq cq c cq c cq c c cq c c c c c	276 abel MP 51646 nmunogl : immun	Score Pred. 15; N caasgftff (1111111) CAASGFTB qmnslrae
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Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, R.K.B.

Eur. J. Immunol. (1992) 22.247.251

Restricted utilization of germ-line V(H)3 genes and short diverse third complementarity-determining regions (CDK3) in human fetal B lymphocyte immunoglobulin heavy chain
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                                                                                                             Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.; Latov, N. J. Meuroimmunol. (1990) 30.245
Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region with anti-myelin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-36, M', 38-62, AR', 67-151 ##label DE2
this sequence has been corrected in reference A60943
#superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                              Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.;
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##note the nucleotide sequence was submitted to the EMBL Data
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#formal_name Homo sapiens #common_name man
02-Dec-1993 #sequence_revision 25-May-1945 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                  Alt, F.W.: Kabat, E.A.; Latov, N.
J. Neuroimmunol. (1990) 26:35-41
Molecular cloning of a human immunoglobulin heavy chain.
variable (V-H) region with anti-myelin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
#formal_name Homo sapiens #common_name man
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain immunoqlobulin homology #label IMM
#length 151 #molecular-weight 16212 #checksum 3341
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Larity 72.8%; Pred. No. 3.22e-77;
Conservative 16; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                  not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heterotetramer; immunoglobulin
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*modified_site pyrrolidone carboxylic acid (Gln) *status
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#journal Proc. Natl. Acad. Sci. U.S.A. (1980) 77:3239-324 #
#title Amino acid sequence of the variable region of a human mu
#cross-references MJID:81013859
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#formal_name Homo sapiens #common_name man
31-Aug-1980 #sequence_revision 23-Oct-1981 #text_change
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T This mu chain was isolated from the plasma of a patient with
                                     #domain immunoglobulin homology #label IMM
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Best Local Similarity 67.2%; Pred. No. 8.57e-77;
Matches 84; Conservative 27; Mismatches 11; Indels
                                                                                                      Length 122;
                                                                                                 Score 684, DB 7; Length 122;
Pred. No. 6.18e-77;
17; Mismatches 12; Indels
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heterotetramer; immunoglobulin
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Local Similarity 74.4%;
Les 93; Conservative
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#map_position 14q32.33-14q32.33
ASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                               #journal Proc. Natl. Acad. Sci U.S.A. (1990) 87-6146-6150
#title Preferential utilization of conserved immunoglobulin heavy
chain variable gene segments during human fetal life.
#cross-references MUID:90349571
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30; Mismatches 12; Indels 3; Gaps
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Ig heavy chain V-III region (Ga) - human
#formal_name Humo sapiens #common_name man
*sequence_revision 23-001-1981 #toxt_change 31-De2-1996
#formal_name Homo sapiens #common_name man
21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
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##residues 1-122 ##label FLO
T This chain was isolated from a Waldenstrom's macroglobulin.
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Biochemistry (1974) 12-2482-2499
The switch point in mu heavy chains of human IgM
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                                                                                                                     Schroeder Jr., H.W.; Wang, J.Y.
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##cross-references GB:M34030
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#accession A02052
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Matches 94; Conservative
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###residoss 1.120 ##label GRI
##erross-references EMBL:218830
FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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##POSIQUES
##CIOSS-references EMBL:246379
FICATION #superfamily immunoglobulin V rugion: immunoglobulin homology
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Embleton, M.J., McCafferty, J., Baler, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.P.; Winter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human anti-self antibodies with high specificity from phage display libraries.
                                     Gladsvkgrftisrdnskntlylgmnslraedtavyyeak-gsmi-vv-aryf-dywaggtl 316
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03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
                                                                                                                                                                                                                                                    S36278 #type fragment
Ig heavy chain V region (clone alpha-THY-23) - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary; nucleic acid sequence not shown
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Best Local Similarity 72.6%; Pred. No. 6.07e-76;
Matches 90; Conservative 19; Mismatches 11;
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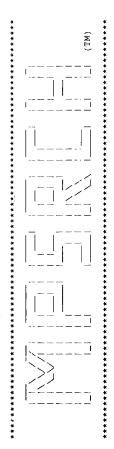
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135 vtvss 139
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M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
Eur. J. Immunol. (1992) 22:247-251
Restricted utilization of germ-line V(H)3 genes and short
diverse third complementarity determining regions (CDR3) in
human fetal B lymphocyte immunoglobulin heavy chain
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##note the nucleotide sequence was submitted to the EMBL Data
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Igheavy chain V region (M74) - human
1gheavy chain V region (M74) - human
1fformal_name How completes from Ending the man
2fformal_name was revision 2l-bec-1990 *text_change
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#formal_name Homo saplons #common_name man
02-Dec-1993 *sequence_revision 26-May-1995 *text_change
                                                                                                                                         3; Gaps
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                                  #domain immunoglobulin homology #label IMM #length 128 #molecular-weight 14474 #checksum
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                                                                                               Length 128;
                                                                                               Score 672; DB 7; Length 128;
Pred. No. 3.10e-75;
14; Mismatches 17; Indels
heterotetramer; immunoglobulin
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nain - human
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S31116
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Local Similarity 73.4%;
nes 94; Conservative
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*superfamily immunoglobulin V region: immunoglobulin homology
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                                                                     Proc. Natl. Acad. Sci. n. S. A. (1990) 87:6146-6150
Preferential utilization of conserved immunoqlobulin heavy
chain variable gene segments during human fetal life.
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15; Mismatches 13; Indels 4: Gaps
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Local Similarity 75.2%; Pred. No. 5.95e-75;
es 94; Conservative 15; Mismatches 11; Indels 5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, June 1992 Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.
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22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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#length 139 #checksum 3756
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                                                            Schroeder Jr., H.W.; Wang, J.Y.
                                                                                                                                                                                                                                                                                              heterotetramer; immunoglobulin
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##cross-references EMBL:214204
                                                                                                                                                                                                                             1-121 ##label SCH
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CLASSIFICATION #superfamily immon
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Best Local Similarity 74.4%;
Matches 93; Conservative
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16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                               #length 121
                                                                                                                                                                                                             ##molecule_type mRNA
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                                Pred.
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            Query Match 72.0%;
Best Local Similarity 72.8%;
Matches 91; Conservative
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Ig heavy chain
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##cross-references NCBIN:54471; NCBIP:64470
##experimental_source X.linked adammad/lobulinemia patients, B
##note sequence extracted from NCRI backbone
FICATION #superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                        *superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *fitle Diversity of immunoglobulin heavy chain gone segment rearrangement in B lymphoblastoid cell lines from X-linked agammaglobulinemia patients.
                                                                                                                                                                                                                  B.D.: Voak, D.: Thorpe, S.: Hughes-Jones, N.C.: Winter, G. submitted to the EMBL Data Library, June 1993. Human antibody fragments specific for human blood group antiqens from a phage display library.
                                                                                                                                                                                                   Marks, J D : Ouwehand, W H.: Bye, T M : Finnern, R.; Gorick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $38493 *type fragment
Ig heavy chain - human (fragment)
#formal_name Homo sapiens #common_name man
06-Jan-1995 #sequence_revision Ub-Jan-1995 #text_change
16-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A49029
1g heavy chain V-11I regainn - human (fragment)
#formal_name Homo sapiens #common_name man
21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
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Berman, J.E.; Alt, F.W.; Schuurman, P.K.
Eur. J. Immuncl. (1991) 21:2355-2353
                                                                                                                                                                                                                                                                                                                                                                                                                         #domain immunoglobulin homology #label IMM #length 123 #checksum 2856
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72.1%; Score 664; DB 7; Length 123;
Best Local Similarity 73.6%; Pred. No. 4.21e-74;
Matches 92; Conservative 12; Mismatches 13; Indels
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##cross-references EMBL:223036
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M.J.D.; Vossen, J.M.; Schuurman, R.K.B.

Pur. J. Immunol. (1992) 22:247-251
Restricted utilization of germ-line V(H)3 genes and short
divorse third complementarity determining regions (CDP2) in
human fetal B lymphocyte immunoglobulin heavy chain
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FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                          1 EVQLLESGGGVVQPARSLRLSAAASGFTFKTYGMHWVRQAPGKGLEWVAGTSFDASNGYY 60
                                                                                                                                         1 grqlvesgggrrgpgrslrlscaasgftfssygmhwrlqapgkglewvaviwydgsnkyy 60
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                                                                      2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region - human
#formal_name Homo sapiens #common_name man
03-Mar-1994 #sequence_revision 10-Nov-1995 #fext_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.
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02-Dec-1993 #sequence_revision 26-May-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain immunoglobulin homology #label IMM #* 132 #m.lacqiar-weight 14606 #.hacksum
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   Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tonnelle, C. submitted to the EMBL Data Library, June 1992
Score 663; DB 7; Length 133
Pred. No. 5.83e-74;
15; Mismatches 16; Indole
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Pelease 2 1D John F. Collins, Riocomputing Pesearch Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:37:11 1998; MasFar time 2.42 Seconds 186.065 Million cell updates/sec Run on:

Tabular output not generated.

(1-125) from US08844215.pep 921 >US-08-844-215-4

IKGRYYLENWGQGILVIVSS 125 1 EVQLLESGGGVVQPGRSLPL Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

56402 seqs, 5095871 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued Database:

1:back1 2.51 3.52 4.53 5.54 6.55 7.56 8.PcT90 9.PCT91 10:PCT92 11:PCT93 12:PCT94 13:PCT95 14:PCT96

Mean 28.138; Variance 145.429; scale 0.193 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No
7	699	72.6	119	7	US-08-331-	Sequence 46, Applicati	1.80e-44
C	999	72.3		۲-	σ	35. Applica	2 160.44
m	657		141	9	-08-25	C.	
4	657	71.3	141	7	US-08-468-	7	,-i
5	652	70.8	125	7	-08-47	99,	4.3
9	650		125	H	PCI-US93-1	ď,	6.27e-43
7	650		125	11	PCT-US93-1	'n	9
80	647	70.2	125	H	PCT-US93-1	ri	1.10e 42
6	641			H	PCT-11893-0	21,	3 370.42
10	638		123	7	US-08-478-	94	5.896-42
11	637	č 69	F.	ς.	TS-08-211-	14	7 100-41
12	632	68.6	122	11	PCT-US93-0	43, A	1.80e-41
13	630	λ. 4	122		U-50811-110d	1.4	2.620-47
14	628	68.2	86	9	US-08-211-	118,	ς.
15		58.2	-1	e-1	PCT-US93-0	12, A	ω.
16		68.1	125	7	US-07-942-	33,	4.58e-41
17			142	7	-308-30-SD	Α	œ.
18		67.8	125	13	PCT-US95-0	76,	8 n2p-41
19			125	7	US-08-276-	76,	8.02
0.3		67.4	17	(1) (1)	PCT-US95-0	(1	1.40e-40
21		67.4	C	۲-	US-08-276-	72,	1.40e-40
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                                                                                                                                                                                                                                      1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                 Gaps
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APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: POGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT TITLE OF INVENTION: ANTIRODIES
                                                                                                                           LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin oTHER INFORMATION: 56P1/CL Variable Heavy chain (V'H)"
NCE 119 Aa; 13279 MM; 79818 CN;
                                                                                                                                                                           / Match 72.6%; Score 669; DB 7; Length 119; Local Similarity 75.2%; Pred. No. 1 80e-44; hes 94; Conservative 16; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
HP 9000/700 Workstation
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35, Application US/07942245 Patent No. 5639641 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/07942245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202) 293-7060
(202) 293-7860
   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHAPACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                        119 amino acids
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                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: ZIVV
                                                                                                                      NAME/KEY: Protein
                                                                  amino acid
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                                                                            STRANDEDNESS
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US-07-942-245-35
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                                                        LENGTH:
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                                                                                                                                                              SEQUENCE
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Ostberg, Lars G. WENTION OF HUMAN MONOCLONAL PRODUCTION PROPURTION: ANTIBOCTION SPECIFIC FOR HEPATITIS H SURFACE ANTIG
                                                                                                                                                                                                                                                                                         61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKDWGW--A-1,F-1,YWGOGT1, 116
                                                                                                                                                                                                                                                                                                            1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYLKSSNKYY 60
                                                                                                                                                                                                                                       Ouery Match 72.3%; Score 666; DB 7; Length 120; Best Local Similarity 74.2%; Pred. No. 3.16e-44; Matches 92; Conservative 15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.40 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Two Samsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08259372A Patent No. 5565354 GENERAL INFORMATION: APPLICANT: Ostberg, Lars G.
                                                                                                 MOLECULE TYPE: peptide
JENCE 120 AA; 13421 MW; 78517 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08259372A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APFLICATION NUMBER: US 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21 AFR:1992 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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FILING DATE: 14-JUN-19
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 21 AFR:19
                                                   120 amino acids
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APPLICATION NUMBER: 15-JUN-1
           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y: USA
94111-3834
                                                                    amino acid
                                                                                        linear
6491103
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                                                                                      TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                           117 VTVS 120
                                                   LENGTH:
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                                                                      TYPE:
                                                                                                                            SEQUENCE
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SECUENCE
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                                                                                                                                                                                                                                                                     61 ADSVKGREIVSRDIVELOMSSLRLEDTAVYYCAIBGSPEGSIKGRYYLENWGGGTL 120
                                                                                                                                                                                                                                                           80 ADSVKGRFTISRDNSKNTLFLQMHSLRAADTGVYYCAKDQLYFGSQSPGHY---WVQGTL 136
                                                                                                                                                                                                                      20 QVQLVESGGGVVQPGRSLELSCAASGFTFSRYGMHWVEQAPGKGLEWVAVISYDGSNKWY 79
                                                                                                                                                                                                                                       1 EVOLLESGGGVVQPGRSLPLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDASNLYY 60
                                                                                                                                                                                                  3; Gaps
                                                                                                                                                                               Score 557; DR 5; Length 141;
Pred. No. 1.70e-43;
9; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 941113834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
OPEPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Pelease #1 0. Version #1 30

CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBEP. US 08/250,372
FILING DATE: 14.JUN-1994
APPLICATION NUMBER: US 07/871,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-1994
JMBER: US 07/871,426
FILING DATE. 31.0CT.1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
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06-JUN-1995
                                                                                                                       LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: protein
JENCE 141 AA; 15613 MW; 114738 CN;
                         RELING DATE: 05-SEP-1986
ATTORNEY/AGENT INFOPMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/POCKET NUMBER: 1182.
TELECOMMUNICATION INFOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08468671.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08468671 Patent No. 5648077
                                                                                  TELEPHONE: (415) 325-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 75.2%;
Matches 94; Conservative
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US-08-468-671-2
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80 ADSVKGPFTISPDNSKNTLFLQMHSLPAARTGVYYCAKDQLYFGSQSPGHY---WVQGTL 136
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Patent No. 568172
GENERAL INFORMATION:
BAPPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
FITLE OF INVENTION: Recombinant Antibodies for Human Therapy NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        11823-50-7
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IIS 07/676,036
                                                                     FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-UNN-1990
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 07/;92,754
                                                                                                                                                                                   APPLICATION NIMBER: HS 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NIMBER: HS 05/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
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JENCE 141 AA; 15613 MW; 114738 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,223
PEFEPENCE/DOCKET NUMBER: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US OF FILING DATE: 05-SEP-1986 ATTORNEY/AGENT INFORMATION:
                                                                   27-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Smith, William M. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIF: 22313-1404
COMPUIER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                      ADDRESSEE:
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                                                             COUNTRY:
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   METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ADSVKGRFTISPDDSKNTLYLQMNSLRAEDTAVYYCAKGQVLYYG-SGSYHWFDPWGQGT 119
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18; Mismatches 18; Indels 2, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Score 652; DB 7; Length 125; Pred. No. 4.32e-43;
                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/478,039 FILING DATE: 07 JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 AA.
                                                                                                                                                                                                                                                012712-160
                                                                                                     APPLICATION DATE: 25-JAN. PRIOR APPLICATION DATA: 07/912,292
APPLICATION NUMBER. US 07/912,292
APPLICATION NUMBER. US 07/912,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                        FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UR 07/735.064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                  APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
                                                                                                                                                              JMBER: US 07/856,281
23-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application PC/TUS9310555 GENERAL INFORMATION:
     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      CHROMOSOME/SEGMENT: 18/2
ICE 125 AA; 13543 MW; 93321 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SILVERMAN, GPEGG J
TITLE OF INVENTION: METHOD FOR
TITLE OF INVENTION: VARIABLE R
                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                          NAME: Teskin Esq., Robin L. REGISTRATION NUMBER: 35,030 REFERENCE/DOCKET NUMBER 011
                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                SS: not relevant
not relevant
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                                                                                                                                                                                                                                                                                                            : 125 amino acids
amino acid
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                                                                                                                                                                                                                                                                              703-836-2021
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide POSITION IN GENOME:
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                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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hes 88; Conservative
                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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VACCINATION WITH A B-CELL SUPERANTICEN AND CONJUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : EVQLLESGGGVVQPGPSIR:SAASGPTFKTYGMHWVPGAPGKGLFWVGGISFDGSNOYY 60
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TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

70.6%, Score 650, DB 11; Length 125;
Best Local Similarity 68.8%, Pred. No. 6.27e-43;
Matches 86; Conservative 20, Mismatches 19; Indels
                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER F0-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5100
INFORMATION FUK SEQ. 1D NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
                                                                                                                                                                                                                                                             UMBER: PCT/US93/10555
29-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKT;
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GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FION: 1..125
125 AA; 13612 MW; 90592 CN;
                                                                                                                                                                                                           PC-DOS/MS-DOS
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                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                  NAME: Howells, Stacy L. REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THEREOF
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                   STREET: 180v ...
CITY: Los Angeles
GTATE: Callfornia
                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                         OPERATING SYSTEM:
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TILLE OF INVENTION: METHOD FOP STIMILATING PRODUCTION OF

TILLE OF INVENTION: VAPIABLE PESION GENE FAMILY PESTRICIED ANTIRODIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYZHA: PC-DÖS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.25
CURPENT APPLICATION DATA:
           ENCE ADDRESS:
E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 550, DB 11, E
pred No 6 27e-43;
20; Mismatches 19;
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29-<u>0</u>CT-1993
4.
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                                                                                                                                                                                                        ATTOPREY/AGENT INFORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION UNMERE: 34,842
REFERENCE/POCKET MIMPER: FD-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (519) 455-5100
TELEPHONE: (519) 455-5100
INFORMATION FOR SEQ. ID NO: 5-
SEQUENCE CHARACTERISTICS:
LENTH: 125 amino acids
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NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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CLONE: KIM
PRATITION
                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 68;
                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE: 29-OCT
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86; Conservative
                                          CITY: Los Angeles
STATE: California
CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
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                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                               linear
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                        ADDRESSEE:
                                                                                    90067
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61 ADSVKGPFIVSPDIVSPDIVET QMSSTPLEDTAVYYCATEGSPFGSTKGPVY-LENWGQGT 119
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Pred No 1 190-42;
18, Mismatches 18, Indols 2, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1 0, Version #1.25 CURRENT APPLICATION DATA:
                                   CORRESPONDENCE ADDRESS:
ADDRESSEE - Spensloy Horn Jubas & Lubitz
STREET: 1880 Century Park Bast - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
WUMMER OF SECTIONCES: 40
COPRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER POLYUS93/10555
FILLING DATE 29-001-1993
CLASSIFICATION
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NAME: Howells, Stacy L.
PEGISTPATION NUMBEP: 34,842
PEPPRENCE/DOCKET NUMBEP: FD-2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application PC/IUS9307832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER PEADABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
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Location: 1 .125
NCE 125 AA; 13464 XW; 94507 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPRY: (619) 455-5100
TELEPAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 69 8%;
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NUMBER OF SEQUENCES.
                                                                                                                                                                                Los Angeles
: Californía
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                                                                                                                                                                                          CITY:
STATE:
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CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPCGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGDGGSTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Recombinant Antibodies for Human Therapy NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE. BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 641; DB 11, L. Pred. No. 3.37e-42; 16; Mismatches 16;
                                                    MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IRM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT:
                                                                                                                                                                                             UMBER: PCT/US92/05126
15-JUN-1992
                                                                                                                   PCT/US93/07832
                                                                                                                                                                                                                                                                                              709P2PCT
                                                                                                                                                                                                                                                                                                                                                                                                       JOGY: linear
122 AA; 13077 MW; 86439 CN;
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Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabii
APPLICANT: Raab, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 94, Application US/08478039
                                                                                                                                                                                                                                   07/934373
                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
                                                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA
APPLICATION NUMBER: PCT/US93
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 70 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                             TELEFAX. 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                               FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              : 122 amino acids
amino acid
                                                                                                                               19930820
                                                                                                                                                                                                                FILING DATE: 15-JUN-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
FILING DATE: 21-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 69.6%;
Local Similarity 72.0%;
es 90; Conservative
                                                                                                                                                                            FILING DATE: 14-JUN-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: F
                                                COMPUTER READABLE FORM:
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            California
                                                                                                                                           CLASSIFICATION:
                          USA
                                                                                                                                 FILING DATE:
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US-08-478-039-94
                                    94080
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                          COUNTRY:
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                STATE:
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61 ADSVKGRFTISRDDSNNTLYMGMNSLRAEDTAVYYCARDRVAVYASVFFIDSFDIWGOGT 120
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                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/47H.u30
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                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATE: 03-MAP-1942
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/71
ATTORNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: TESKIN ESG., ROBIN L. REGISTRATION NUMBER: 35,030 REFERENCE/POCKET NUMBER: 012712-160
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                         IUMBER: US/08/478,039
07-JUN-1995
                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
APLICATION MOMBER: US 08/379,072
PRIOR DATE: 25-JAN-1995
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 141, Application US/08211202 Patent No. 5565332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 141, Application TS, 79211202.
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                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 23-MAP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 123 amino acids
amino acid
                                 COMPUTER READABLE FORM MEDIUM TYPE: Floppy disk
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  USA
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                                                                           COMPUTER:
COUNTRY:
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OPERATING SYSTEM:
SOFTWARE: DATANT
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David W. Clough, Marshall O'Toole Gerstein Murray &
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     APPLICANT: JESPERS, Laurent Stephane Anne Therese APPLICANT: WINTER, Gregory Paul TITLE OF INVENTION: Production of chimeric antibodies - a TITLE OF INVENTION: combinatorial approach NUMBER OF SEQUENCES : 144
CORRESPONDENCE ADDRESS:
                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPEPATING SYSTEM. PC-DOS/MS-DOS SOFTWARE: Patentin Release #1 0, Version #1 25 (EPO) CURPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 637; DB 6; Length 116;
Pred. No. 7.10e-42,
16; Mismatches 13; Indels
                                                                              6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                        28111/31960
                                                                                                                                                                                                                                                                                                                      APPLICATION NIMBER PCT/GR42/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: DAVID W. Clough
REGISTRATION NUMBER 36 107
REPERENCE/POCKET NUMBER: 28111/3196(
                                                                                                                                                              23-SEP-1992
N: 435
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                                                                                                                                                                                                       PRIOR APPLICATION DATA.
APPLICATION NUMBER. GR 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA.
APPLICATION NUMBER: GR 9120377.8
FILING DATE: 25-SEP-1991
                                                                                                                                                                                                                                                                      GR 9206318 9
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116 AA; 12678 MW; 72426 CN;
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TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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INFORMATION FOR SEQ ID NO: 141:
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APPLICATION NUMBER: GR 92
FILING DATE: 24-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                     : 116 amino acids
amino acid
APPLICANT: BAIER, Michael
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Best Local Similarity 73.7%.
87; Conservative
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                                                                                     Chicago
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PCT-US93-08435-43
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                                                                                                         COUNTRY:
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APPLICANT: the Navy
APPLICANT: to S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Conferring Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
COPPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PDIVIGRPIISEDNSKNILYLDANNSLPAEDIAVYVARLIY-VG-YLG-VAMEVWOGGIL 117 : 1:1 | 1:1 : 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:
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Pred. No. 1.80e-41;
15; Mismatches 18; Indels 3; Gaps
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SOTTWARD: Patentin Palease #1.0, Vorsion #1.25
CURRENT APPLICATION DATA:
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                                                                                                       Sequence 43, Application PC/TUS9308435
SENFEL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation APPLICANT: U.S. Government, Secretary of
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x 457, 321 Norristown Foad
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PEFERENCE/DOCKET NUMBER: SRC P50107
FELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
AITOFNEY/AGENI INFORMATION:
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Sequence 43, Application PC/TUS9308435.
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SEQUENCE 122 AA; 13313 MW; 87403 CN;
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IBM PC compatible
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INFOPMATION FOR SEC ID NO: 43:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy of
COMPUTER: IBM PC comp
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Best Local Similarity 71.2%;
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Box 457, 32
CITY: Spring House
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APPLICANT: U. S. Government, Secretary of APPLICANT: the Army TITLE OF INVENTION: Novel Antibodies for Conterring Passive TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSEISDGGSYTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.4%; Prod. No. 2.62e-41;
Matches 88; Conservative 16; Mismatches 18; Indels 3;
                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPANDS
OPERATING SYSTEM. PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 AA
                        APPLICANT: SmithKline Beecham, Corporation APPLICANT: U. S. Government, Secretary of APPLICANT: the Navy
                                                                                                                                                                                                                                                                                                                                                                                    NAWE: Bak, Mary E.
REGISTRATION NUMBER. 31,215
REPERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION.
TELEPHONE: (215) 540-9200
TELEPAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            E: Howson and Howson
Box 457, 321 Norristown Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPT
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US93/08435
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 118, Application US/08211202
Patent No. 5565332
Sequence 14, Application PC/TUS9308435 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
122 AA; 13329 MW; 88138 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 118, Application US/08211202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDAPD:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
                                                                                                                   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                      Spring House
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                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                               USA
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                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                    STATE:
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1 QVOLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
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APPRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray & ADDRESSEE: Borun
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HOOGENBOOM, Hendricus Renerus Jacobus Matteus
                                                                                                                                                                                       MEDIUM TYPE: Floppy disk compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: US/C8/211,202
             APPLICANT: BAIER, Michael
APPLICANT: BAIER, Michael
APPLICANT: JESPERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies
TITLE OF INVENTION: combinatorial approach
UNDRER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 628: DR 6; Length 98;
Pred. No. 3.80e-41;
11; Mismatches
                                                                                                                      6300 Sears Tower, 233 South Wacker Drive
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FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER. GB 9206372.6
                                                                                                                                                                                                                                                        UMBER. US/08/211,201
23-SEP-1992
                                                                                                                                                                                                                                                                                                         TUMBER. GB 9120252.3
23-SEP-1991
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JENCE 98 AA; 10838 MW; 50043 CN;
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                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92
FILING DATE: 24-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312-474-6300
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APPLICATION NUMBER OB
FILING DATE:
PRIOR APPLICATION NUMBER:
GRAPHICATION NUMBER:
GRAPHICATION NUMBER:
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INPORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 3
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Best Local Similarity 83.5%;
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                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                        Chicago
                                                                                                                                                             USA
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      APPLICANT:
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                                                                                                                                                                COUNTRY:
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APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: U. S. Government, Secretary of
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Conferring Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ADSVKGRFIVSRPNSRDTVFLQMSSLRLEDTAVYYCATEGSPFGSIKGRYYLENWGGGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PDIVIGRETISPONSKNILYLQMNSLPAEDTAVYYCAKLIY-YG-YDG-YAMDYWGQGIL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVKQAPGKGLEWVAGISFDGSNQYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19477
COMPUTER PEADAPLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
PEPERENCE/DOCKET NUMBER: SEC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEPHONE: (215) 540-9200
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Howson and Howson
Box 457, 321 Norristown Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                        Sequence 12, Application PC/TUS9308435 GENERAL INFORMATION:
                                                                                                                    Sequence 12, Application PC/TUS9308435.
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MOLECULE TYPE: protein
SEQUENCE 122 AA; 13370 MW; 87746 CN;
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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STATE:
01-JAN-1909
\texttt{E} \overset{\mathsf{A}}{\times} \overset{\mathsf{A}}{\times} \overset{\mathsf{A}}{\circ} \overset{\mathsf{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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Search completed: Tue Feb 24 07:37:23 1998 Job time: 12 secs.

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Release 2.1D John F. Collins, Biocomputing Fesearch Jnit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07-10:11 1999, MasPar time 7.49 Seconds 231.859 Million cell updates/sec Run on:

Tabular output not generated

>US-08-844-215-4

Description: Perfect Score: Sequence:

TKGRYYLENWGQGTLVTVSS 125 (1-125) from USG8844215.Pep 921 1 EVQLLESGGGVVQPGRSUR...

PAM 150 Gap 11 Scoring table:

111726 seqs, 13889129 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-genesed30 Database:

| part| 2 part2 3 part3 4 part4 5.part5 5 part5 7:part7 8:part6 9:part9 10:part10 11:part11 12:part12 13:part13 11:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23

Mean 30.277; Variance 155.246; scale 0.195 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	ΩI	Description	Pred. No
1	069	74.9	. 0	7		Sequence of the heavy	1.13e-45
2	581	ω,	123	23	W13531	Anti-melanoma antibod	6 15e-45
m	680	73.8		7	P12134	ORF 3 of 489 human MA	7.43e-45
4	677	3.	123	23	W15534	Anti-TGF beta-1 scFv	1 300-44
ľ	674	73.2	4	13	R75392	Anti-interleukin-1-al	2.29e-44
9	699		119	α: • •	R95216	Human foetal immunoq1	5.850-44
7	668	ς.	123	23	W15535	Anti-TGF beta-1 scFv	7.07e-44
<b>6</b> 0	999	72 3	115	4	P22571	Heavy chain VH3 5 fro	1 036-43
6	666	C1	120	17	P52064	Heavy chain variable	1.036-43
10	657	71.3	141	19	W01522	Monoclonal antibody F	5.57e-43
11	657	71.3	٦		W24984	Monoclonal antibody P	5.57e-43
12	653	70.9	7	7	W13524	Anti-melanoma antibod	1.18e-42
13	651	70.7	143	o,	R54047	Sequence of the VH re	1.72e-42
14	550	7 Û E	125		P54788	SpA-reactive IgM heav	2 070-42
15	650		125		P54789	ΧbΙ	2.076-42
16	649	70.5	123	C.1	WIFERS	Anti-TGF beta-1 scFv	2 500-42
17	639		111		P12275	Anti-human Php HAM-R	1.530-41
18	638	59.3	124	۳: دع	W13537	Anti-melanoma antibod	1 976-41
19	638	69.3	125	σ.	P54784	SpA-reactive IgM heav	1.970-41
20	638	69.3	140	14	P894R0	Anti-human IL-4 human	1 976-41

97e-	.86e-4	.16e-4	.02e-4	0.50-4	29e-4	80e-4	, <u>0</u> 6e-4	1060-4	.28e-4	299-4	28e-4	540-4	.54e-4	.86e-4	.86e-4	- 4	.71e-4	.71e-4	71e-4	.260-4	94e-4	.75e-4	.75e-4	6.90e-40
numan IL-4 hum	chain wariab	immunoale	chai	anised heary cha	KOL heavy chain.	anised	lanoma	ti-HBs he	Anti-human Phr PEG-A	Anti-TGF beta-2 scFr	anised heavy :	iable region o	-109	Poeta-2 s	man anti	ntibody HSV8	Sasas	-	region of H	2 human	Human TNF binding ant	egion of HIV	F-HIV G	17
R80617	t -	(1 (0)	500	5	361	331	353	305	122	50	13.	318	523	552	50	565	277	623	25.5	146	000	125	(1	774
14	Ľ	C1	Œ)	CT:	7	c.	<u>~</u> 1	œ	C 4	C1	œ.	<b>~</b> 1	C.	23	C1	23	9	0	۲.	ထ	ų,	19	0	4
467	ć.	-	5.5	Ci	C1	CI	CI	in		-	CI	C÷	C +	$\overline{}$	C 4	4	C1	C1	Ci	77	$\overline{}$	N	C 4	C4
69.3	ď.	an on	α,	a'i	œ	ď	m m	ω	σ,	0)	80	α;	α.	a)	α)	۲.	۲.	۲-	7	7	٠.	7	۲-	7
538	( )	(*)	~)	~	C.	C,	04	(1	11	(1	C 1	CI	CI	C1	(1	C1	C 1	C 4	(1	0.1	C1	$^{\circ}$	C 1	e 1
21	(1 (1	(C)	ដី	C.I	3.6	27	28	953	() (*)	31	32	33	2.4	n)	36	37	38	39	C: ₹7	e 1 =#	C.	43	77	44 N

# ALIGNMENTS

AC DE DE KW	NOGIOI SCANDAIU, FICCEIII, 176 AM.
⊢យ១៥៤	R38161;
មានាមិ≱	01-OCT-1993 (first entry)
១២≥	
医区	immunoglobulin G3 (1963) produced by transformed human R-cell line
3	88BV59, ATCC CRL 10624.
	B-cell; immunoglobulin q; cancer; tumour.
SO	iens.
FH	Key Location/Qualifiers
FT	lon
FT	- VAR
FI	/note= "1st AA is denoted AA#1"
FT	Region 3149
FT	/label= CDR 1
E-	Region 5094
FT	/label= CDR 2
←	Pagin 95 .111
FT	/label= CDR 3
FT	Region 112223
FI	/label= CH 1
FT	Region 224238
FI	/label= Hinge
H	Region 239242
FT	/label= Fab'
Nd	EP-546634-A
PD	16-JUN-1993.
PF	
PF	
FA	~
Ĩd	Crichton VZ, Haspel MV, Kobrin BJ;
α.	-190015
E G	N-FSDB, Q43772.
FT	an B.cell line
PT	
Ęı	is actively immunised with autologous tumour anti
PŢ	
(r)	Claim 5. Fig 2: 18pp. English.
رو	043772 encodes the complete heavy chain from the leader through AAs
ţ	THE ARBY ONCH THE MANAGEMENT OF THE PARTY OF
, (	Contract asses virtue and
	()
Ç	mutation. It is radically different from any germ line D region. It
ت	utilises germ line 183 It is of note that a overeine at AA nosn
ر	(An No. 78 in 528161) is prosent within the 888050 VP No other

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c antibodies has been produced. The process involves: (a) constructing at antibodies has been produced. The process involves: (a) constructing at antibodies has been produced. The process involves: (a) constructing at antibodies has been produced. The process involves: (a) constructing at the place of the place of the place in the place in the place in the place in a cancer patient; (b) screening for anti-tumour antibodies in the phage library in a binding assay with cultured tumour cells of the absorption adainst normal human cells; (d) conding the phage selected in the place in the place with at least two types of cultured normal cells; and c); (e) assaying the specificity of cloned phage by step (b) and (c); (e) assaying the specificity of cloned phage that do not bind conclude the place with a feast two types of cultured normal cells; or cultured tumour cells derived from more than one other tumour that is concluded the place in the place in the place in the place in the place of continuour cells derived from more than one other tumour that is concluded as described above. The antibodies produced can be used for a method as described above. The antibodies produced can be used for chain antibodies have low immunogenicity in humans compared to murine monocolonal antibodies (Mabs). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a cumour cell inne can be improved by genetic manipulations.
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O
                                                                                                                                                                                                                                                                                                     61 ADSVKGRFIVSRDNSPTVFLQMSSLRLEDTAVYYCATEGSPFGSIKGRYYLENWGOGTL 120
                                                                                                                                                                                                                                                             80 adsvkgrftisrdnskntlylgmnslraedtavyycvkegfgsvvvithlafdvvgggtm 139
                                                                                                                                                                            20 qvqlvesgggvvqpgrslrlscaasqftfssygmhwvrqapgkgldwvavisydgsneyc 79
human variable region heavy chains have a cysteine at this posn. i.e. Kabat posn. 59.
Sequence 192 AA;
                                                                                                                                                                                                                   1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-melanoma antibody héavy chain clone V575.
Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
cancer; tumouriqenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prodn. of human monoclonal anti-tumour antibodies - by screening a tusion phage library produced using peripheral blood lymphocytes from a cancer patient
                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 73.9%; Score 681; DB 23; Length 123;
Local Similarity 73.6%; Pred No 4 15e-45; Indels 3
hes 92; Conservative 18; Mismatches 12; Indels 3
                                                                                        Score 690; DB 7; Length 192;
Pred. No. 1.13e-45;
                                                                                                                                  17; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            r 2
W13531 standard; protein; 123 AA.
                                                                                                 Query Match
Best Local Similarity 72.8%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-497647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50..66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-1996; IB1032.
30-JUN-1995; US-4976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        garen A;
97-109061/10.
                                                                                                                                                                                                                                                                                                                                                                 140 vtvss 144
                                                                                                                                                                                                                                                                                                                                                                                                           121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
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18; Mismatches 12; Indels 3: Gaps

Matches

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307 adsvkgritisrdnsrdmlyvqmnslraedtavyycakekes qq--seysfdywaqqtl 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 gyglvesgggvvgpgrslrlscaasgftfrsygmhwyrgapkglewvavissdgsydyy 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLLESGGGGVVQPGRSLPLSCAASGPTFKTYGMHWVRQAPGKGLFWVAGISFDGSNOYY 60
                                                        61 adsvkgrftisrdnskkntlylgmnslraedtavyycar-gipygg-nsdygmdvwdhgt 118
                                                                       12: Indels 3; Gaps
1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Fig 18; 104pp; English.
This sequence is derived from the nucleotide sequence encoding the heavy chain variable region. The "x" residues represent nonsense codons. The coding sequence has been translated in all 3 reading frames (see also R1213 and R12133).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MOV-1997 (first entry)
Anti-TGF beta-1 scFv antibody 1-B2 VH domain.
Aransforming growth factor beta-1; TGF-beta-1; human;
antibody engineering; scFv. phaye display; hung tibrosis;
arterial injury; proliferative retinopathy; retinal detachment;
adult respiratory distress syndrome; liver cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligomeric immunoglobulin(s) with high avidity for antiqen(s) formed by duplicating esp. variable region of light chain of 196
                                                                                                                                                                                                                                               01-AUG-1991 (first entry)
ORF 3 of 489 human MAb heavy chain variable region; duplication;
immunoglobulin G; heavy chain; variable region; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Match 73.8%; Score 680; DB 2;
Local Similarity 76.0%; Pred. No. 7.43e-45;
les 95; Conservative 16.
                                                                                                                                                                                                                                                                                                                                                                 /note= "last 3 residues of leader and variable
                                                                                                                                                                                                                                                                                                                                                                         region; the rest of leader is translated in ORF 1"
                                                                                                                                                                                                                                                                                           passivé immunity; group B streptococci.
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
244..369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W15534 standard; Protein; 123 AA.
                                                                                                                                                                                                           T
R12134 standard; Protein; 505 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shuford WW, Harris LJ, Raff HV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1989; US-432700
                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-1990; U06426
                                                                                                                                                                                                                                                                                                                                                       /label= L'V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91-163947/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 vtvss 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VTVSS 125
                                                                                                                                119 qvtvs 123
                                                                                                                                                            120 LVTVS 124
                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                      W09106305-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W15534
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This polypeptides sequence comprises the VH domain of human scrv antibody 182 (also known as 7A3), which is specific for antibody 182 (also known as 7A3), which is specific for antibody 182 (also known as 7A3), which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (TG0380) isolated from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see W1552-40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative inver cirrhosis, post myocardial infarction, post-angioplasty restenosis, scleroderma, vascular disorders, cataract, glaucoma, or setenosis, scleroderma, vascular disorders, cataract, glaucoma, or steporosis), or (ii) immune and inflammatory diseases (theymatorid arthritis, macrophage deficiency diseases or macrophage pathogen infarting and VL can be infection). Nucleic acids encoding human antibody VH and VL can be infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 adsvkgrftisrdnskntlylqmnslraedtavyycaktge-ysgydssg-vdvwgkgtt 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ADSVKOPFIVSPDAVSPDAVSPDAVSCHLEDIAVYYCATEASPFGSIKGPYYLENWSGSTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 qvqlvesgggvvqpgrslrlscaasgftfssygmhwvrqapgkglewvavisydgsnkyy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agent contg. antiquen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, \rho g for central of fibresis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used for prodn. of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5
            scleroderma; vascular didease; cataract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease; macrophage pathogen infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R75393.
04-NOV-1995 (first entry)
Anti-interleukin-1-alpha human monoclonal antibody VH segment.
Monoclonal antibody, interleukin-1-alpha, eytekine,
antiinflammatory; prophylactic; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 73 5%; Score 677; DB 23; Length 123;
Local Similarity 73.6%; Pred: No. 1.30e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
post myocardial infarction; post-angioplasty restenosis;
                                                                                                                                                                                                                                           Tohnson KS, Pope AB;
                                                                                                                                                                                                                                         Bacon L. Green JA, Jackson PH, Tohnson KS, Pope .
Tempest PR, Thompson JE, Vaughan TJ, Williams AJ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 15,
                                                                                                                                                                              19-JAN-1996, GB-001081.
06-OCT-1995, GB-020486.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      k (FP) 1 (+1 to +30)"
50, 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nM) and low IC50s for neutralisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide 1.19
/note* "signal peptide"
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                                                                                                                                     23-APR-1997
07-OCT-1996; 020920
                                                                                                                                                                                                                                                                                                     97-215360/20.
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                                                                                                                                                                                                                                                                                                                             N-PSDB; T60380
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                                                                                                   Homo sapiens.
GB2305921-A
                                                                                                                                                                                                                                                                                      Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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  qq
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80 aesvkgrftisrdnsknilflygndslæledlævyvoar yrpkvvipap Habwyyytl 126 Hilli Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the variable heavy chain segment of a human monoclonal antibody (HuMAb) against interleukin-1-alpha. The MAb is of subclass 1gG4 and binds to lymphokines/monokines with an affinity of 10(9)/M. The Mab or fragment (FV, single-chain FV, Fab or F(ab') is used in the treatment of inflammation e.g. rheumatoid arthritis, osteoarthritis and inflammatory bowel diseases, and in the treatment or psortal inflammatory bowel diseases, and in disease and tumours. The MAb or fragment can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVULLESGGGVVÜPGRSLFLSCAASGFTFKTYGMHWVRUAPGKGLEWVAGLSFDGSNUYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 574, DB 13, Length 141;
Pred. No. 2.29e-44;
15; Mismatches 15; Indels 3: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 grglvesggggvrgpgrslrlsctasgftfsmfgrhwrrgspgkglewraansydgsakyy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human monoclonal antibody against a human cytokine - used to mfr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Djossou O, Fossiez F, Garonne P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            medicament to treat inflammation.
Claim 7; Page 44-45; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .m. 6
R95216 standard; protein; 119 AA.
R95216;
                                                                                                                                                                                                                 "CDP 3 (+99 to +110)"
                                                                                                                                                                                                                                                                    "JH 1 (+111 to -122)"
                                                                                                       "CDR 2 (+50 to +66)"
86..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cuery Match
Best Local Similarity 73.6%;
Matches 92; Conservative
"CDR 1 (+31 to +35)"
55..68
                                                                                                                                                          "FR 3 (+67 to +98)"
118 129
                                                "FR 2 (+36 to +49)"
                                                                                                                                                                                                                                             130.141
                                                                                                                                                                                                                                                                                                                                                                                                           (SCHE ) SCHERING-PLOUGH. (SCHE ) SCHERING CORP.
                                                                             85
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28-OCT-1994; US-331396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WFI; 95-206937/27.
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09-MAY-1996.
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Example 13: Figure 11A; 116pp; English.

Example 13: Figure 11A; 116pp; English.

A novel recombinant DNA molecule which encodes a single chain fusion protein or antibody comprising the FV region of both the light and heavy chains of an antibody (Ab) fused together, and an effector molecule, where the fusion protein or Ab has the binding specificity of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production of such fusion proteins or antibodies. The fusion proteins can be used in compositions as an immunotoxin to inhibit tumour cell growth the single chain antibody can be used to detect the presence or The single chain antibody can be used to detect the presence or patient. The antibodies are also useful as multiple targetting moleties, providing at least 2 kinds of biological activity. They moleties, providing at least 2 kinds of biological activity. They can also be used in diagnostic assays and for the imaging of tumours when attached to a radiolabel and for the pathological diagnosis of tumours. Humanised antibodies are less immunogenic than the mouse was an and by the mouse that the mouse and the mouse of the pathological diagnosis of the pathological diagnosis of the pathological pathological diagnosis of the pathological control of the mouse that the mouse of the pathological diagnosis of the pathological diagnosis of the pathological control of the pathological control of the pathological control of the pathological diagnosis of the pathological diagnosis of the pathological diagnosis of the pathological diagnosis of the pathological control of the pathological control of the pathological diagnosis of the pathol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 qvelvesgggvvqpgrslrlscaasgftfssyamhwvrqapqkglewvavisydgsnkyy 60
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72.6%; Score 669; DR 18: Length 119;
Best Local Similarity 75.2%; Pred. No. 5.86e-44;
Matches 94; Conservative 16; Mismatches 9; Indels 6; Gaps
                                                                                                                - useful to diagnose and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-TGF beta-1 scrv antibody 31G9 VH domain. Anti-TGF beta-1 scrv antibody 31G9 VH domain. Transforming growth factor beta-1; TGF-beta-1; human; antibody engineering; scrv; phage display; lung fibrosis; arterial injury; proliferative retinopathy; retinal detachment; adult respiratory distress syndrome; liver cirrhosis; post myocardial infarction; post-angioplasty restenosis; scleroderma; vascular didease; cataract; glaucoma; scarring; glomerulonephritis; actophorosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease;
                                                                                                                                     treat cancer, specifically bind Lewis(Y) related carbohydrate
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                               [,ee B:
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Benhar I, Brinkmann U, Fitzgerald D, Jung S,
                                                                                                                      Single chain fusion proteins and antibodies
                                                        Pai L, Pastan I, Willingham M; 462/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W15535 standard; Protein; 123 AA.
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19-JAN-1996; GB-001081.
06-0CT-1995; GB-020486.
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                                     Benhar I, Brink
Padlan EA, Pai
WPI, 96-251462/2
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claim 16; Fig 1a(11): 184pp; English.

This polypeptide comprises the VH domain of human scryv antibody
20 31G9, which is specific for transforming growth lactor (7GF)
21G9, which is specific for transforming growth lactor (7GF)
21G9, which is specific for transforming growth lactor (7GF)
21G9, which is specific for transforming growth lactor of human soft human control is ingle chain Fv library. The antigen-hindron domains of human context the adverse effects of TGF beta, such as (1) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, of fibrosis dault respiratory distress syndrome, liver cirrhosis, post adult respiratory distress syndrome, liver cirrhosis, post upcompande deficiency adactors, cataract, glaucoma, or esp. neural scarring and pomerulomephritis, also (not claimed) osteoporosis, or (11) manne and inflammatory diseases (e.g. rheumatoid arthritis.

Nucleic acids encoding human antibody VH and VL can be used for prodn. of recombinant antigen-binding domains. These are highly and low 1050s for neutralisation.

Sequence 123 AA:
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Heavy chain VH3.5 from BSA binding scFv fragment.
Heavy chain VH3.5 from BSA binding scFv fragment; coat:
Fd; bacteriophage, gene III; filamentous; phagemid; capsid; coat:
pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
specific binding pairs; replicable genetic display package; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            producing members of specific binding pairs - by expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
72.5%; Score 668; DB 23; Length 123;
Best Local Similarity 73.5%; Prod No 7 07e-44;
Matches 92; Conservative 15; Mismatches 16; Indels 2
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15-MAY-1991; GB-010549.
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12-NOV-1990; GR-024503.
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Table 11; Page 1
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120 AA;

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Method of resurfacing of rodent antibodies to produce humanised antibody forms - for producing non-human antibodies with improved therapeutic efficiency by presenting human surface on V-region Example 1, Fig 4B, 230pp; English.

Modification of a rodent antibody (Ab) or fragment by resurfacing in order to produce a humanised rodent Ab can be determined by calculating homology between murine and human Ab antibody surfaces. In order to test the resurfacing approach of the invention, three humanisation experiments were set up: (1) traditional loop grafting, (2) resurfacing approach using most similar chain; and (3) resurfacing approach using human sequences with most similar surface residues. The Ab used was the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-N901 Ab (see R2004). Experiment 2 was carried out using the present sequence which represents the human G36005 Ab heavy chain variable region with 89 percent homology with anti-Na01 Ab N901/G36G05 (P52065) was prept. by CDR grafting. Sequence numbering starts at 11% in the
                                                                                                                                                                                                                                                                                                                           1 qvqlvqsqqqvvqpqrslrlscaasqftfssygmhwvrqapgkqlcwvavisydqsnkyy 60
                                                                                                                                                                                                                                                                                                                                                               1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                      61 adsvkgrftisrdnskntlyjqmnslraedtavyycaktg--yssgwg-yf-dywgggt 115
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ADSVKGRFIVSPONSPOTVFLQMSSLPLEDIAVYYCATEGSPFGSIKGPYYLENWGQGT 119
                                                                                                                                                                                                                                                                                     4; Gaps
96 clones analysed, 43 showed binding to both phox:RSA and BSA. Thirteew were designated BSA binders. Thirteen of fourteen clones sequenced had the same sequence, the VH derived from a human VH3 family gene (shown here) and the VL from a human VH4 family gene (R2552). The other was derived from a human VH4 family gene and a human VH4 family gene. One clone bound only to phox:BSA (oxazolono binder). This sequence revealed a VH derived from a human VH1 family gene (R22569) and VL from a human V lambda I family gene (R2550). See also P21560.307, 309.312, P22450, P22565, P22567.81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-007-1996 (first entry)
Heavy chain variable region of human G36005 antibody.
antibody, humanised; murine; human; heavy chain; light; variable; framework region; complementarity determining region; reshaping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pees AP, Poguska MA, Searle SMJ;
                                                                                                                                                                                                                                          // Match 72.3%; Score 666; DB 4; Length 115; Local Similarity 75.6%; Pred. No. 1.03e-43;
                                                                                                                                                                                                                                                                                 15, Mismatches 10, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= complementarity_determining_region_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modelling; surface residue; modify.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R52064 standard; Protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label = framework_region_1
                                                                                                                                                                                                                                                                                   90, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pedersen JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-942245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36..49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEDE/) PEDERSEN J T. (IMMU-) IMMUNOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-1993; 307051,
09-SEP-1992; US-942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94-120230/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "CDR 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "CDR 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "CDR 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "FR 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "FR 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP-592106-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note- "FR 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guild BC,
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R52064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                   Matches
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diseases caused by infection with hepatitis. B have been prepared from a cell line obtained by fusing a xenogeneic hybridoma designated SPAZ 4 with blood cells of a patient, immunised with hopatitis P vaccine. Specific antibodies are PELT ZML-1, ZML-2, MD3-4 and LN3-3, each of these being of the 19G1 class. The present sequence is the heavy
                                                                                                                                      61 adsvkgrftisrdnskntlylqmnslraedtavyycardrkdwgw--a-lf-dywgggtl 116
                                                               1 gvglvesgggvvqpgsslrlscaasgftfssyambwrrqapgkglewravisydgsnkyy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A FORTH MAN MONOTORIAN AND A SPECIFIC FOR hepatitis B surface antigen are used to treat or prevent infection of in diagnostic assays Claim 4; Column 27-28; 26pp; English.

Monoclonal antibodies effective for the diagnosis and treatment of
                                                                                          1 EVOLLESGGGVVOPGPSFPLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDGSNOYY 60
                                 4; Saps
                                                                                                                                                                                                                                                                                                    03-MAR-1997 (first entry)
Monoclonal antibody PEL-1 heavy chain variable region.
Monoclonal antibody; diagnosis; treatment; infection; hepatitis B;
xenogeneic hybridoma; SRAZ 4; PEL-1; ZM1-1; ZM1-2; MD3-4; L03-3;
IgGl class, heavy chain, light chain, variable region.
Score 666; DB 17; Length 120; Pred. No. 1.03e-43; 15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label* complementarity_determining_region_l
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                            T 10
W01522 standard; Protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "start of FR3 region"
Query Match
Best Local Similarity 74.2%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label = framework_region_l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130..141
                                                                                                                                                                                                                                                                                                                                                                                                                                              Region 20..11/
/label= V_H(III)_region
                                                                                                                                                                                                                                                                                                                                                                                                                            /label= leader_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-1986; US-904517.
31-OCT-1986; US-925196.
11-MAY-1988; US-192754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.JUN-1990, US-538796.
27-MAR-1991, US-676036.
21-APE-1992; US-871426.
14-JUN-1994, US-259372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50..53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70..85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-1986; 904517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= J_H4_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 96-476304/47.
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                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                   117 vtvs 120
                                                                                                                                                                                                               121 VTVS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "CDR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "FR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= FR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ostberg LG;
                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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8888888888
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Monoclonal antibody PEL-1 Wh region. human; monoclonal antibody.
Heavy chain; light chain; variable region; human; monoclonal antibody;
immunisation; hepatitis B virus; HBV; vaccine; mouse; fusion; xenogeneic;
peripheral blood lymphocyte; surface antiqen; cell culture; ion exchange;
chromatography; size separation; primer; PCR; polymerase chain reaction;
amplification; hybridoma; infection; immunosuppression; hepatitis:
liver transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of hepatitis B - with human monoclonal antibody
Example 8: Column 15-18; 25pp; English.

Example 8: Column 15-18; 25pp; English.

This is the amino acid sequence of the heavy chain variable (Vh) region from the human monoclonal antibody (MAD) PEI-1. The MAD was generated by immunising humans with a hepatitis B virus (HRV) varcine, isolating peripheral Brood lymphocytes (PPL) and fusing them with a mouse/human xenogeneic cell line SPAZ-4. 5 cell lines were isolated: PFI-1, ZMI-1, ZMI-2, MD3-4 and LO3-3. The cell lines were then tested for production of an anti-hepatitis B virus surface antigen antibody by ELISA The MADs are then purified from large scale cell culture by protein A chromatography, size separation on Sephacryl S300 qel and ion exchange
                                                                                                                                                                                                                                                    80 adsvkgrftisrdnskntlflqmhslraadtgvyycakdqlyfgsqspghy---wvqgtl 136
                                                                                                                                                                                                                                                                                 1 EVOLLESGGGVVOPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                             20 qvqlvesgggvvqpgrslrlscaasgftfsrygmhwvrqapgkglewvavisydgsnkwy 79
                                                                                                                      3; Gaps
                                                                           Score 657; DB 19, Length 141;
Fred No 5 57e-43.
                                                                                                                      Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "complementarity determining region 2"
                                                                                                        Fred No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W24984 standard; Protein; 141 AA.
                                                                                                                             6
                                                                             Query Match
Best Local Similarity 75.2%.
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130..141
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"VhIII region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-192754.
US-538796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-1991; US-676036.
              variable chain of PE1-1. Sequence 141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20..141 "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-904517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-925196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-1994; US-259372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-871426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69..85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            904517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Jh4 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SANO ) SANDOZ LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "D region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; T85838
                                                                                                                                                                                                                                                                                                                                                            137 vtvss 141
                                                                                                                                                                                                                                                                                                                                                                                                     121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS5648077-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ostberg LG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W24984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
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Claim 19; Page 62: 87pp; English.

A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphocytes (PBLS) of a cancer patient; (b) screening for anti-tumour antibodies in the phage library in a binding assay with cultured unmour rolls of the same type as the patient; (c) removing extraneous antibodies in same type as the patient's tumour; (c) removing extraneous antibodies in incubating the phage with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phage that do not bind and (f) further testing the specificity of coloned phage that do not bind to either cell line of cultured normal cells in further binding assays to cultured tumour cells derived from more than one other tumour that is
chromatography on Q-Sepharose. The heavy and light chains of the Mabs were isolated and their amino acid sequences determined. Primers were generated and used to amplify cDNA synthesised from RNA purified from accordance of the heavy and light chains (nucleic acid and amino acid) from Mabs PEI 1, 2Ml 1, 2Ml 2, and MNS-4 shown in 185838-45 and W2494-91. The Mabs PEI 1, 2Ml 1, 2Ml-2 and MNS-4 brown in infections in immunosuppressed patients or patients with chronic active hepatifis, especially liver transplant patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not the patient's tumour. The present sequence represents a human heavy chain antibody, from an scFv antibody tusion phage library, produced by a method as described above. The antibodies produced can be used for diagnostic and therapeutic applications and for isolating tumour antigens for studying tumouriquenesis of for use as anti-cascer vaccines. The human antibodies have low immunogenicity in humans compared to murine monoclopial antibodies (MAbb). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 adsvkgrftisrdnskntlflgmhslraadtgvyycakdqlyfgsgspqhy---wvgqtl 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ADSVKGRFIVSRDNSRDTVFLQMSSLRLEDTAVYYCATEGSPFGSIKGRYYLENWGQGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 qvqlvesgggvvqpgrslrlscaasgftfsrygmhwyrqapqkqlewvavisydqsnkwy 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNOYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches 19; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-melanoma antibody héavy chain clone V86.
Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prodn. of human monoclonal anti-tumour antibodies - by screening a
fusion phage library produced using peripheral blood lymphorytes
from a cancer patient
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 71.3%; Score 657; DB 23; Length 141; Best Local Similarity 75.2%; Pred. No. 5.57e-43; Matches 94; Conservative 9; Mismatches 19; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; tumourigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 97-109061/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- CDR1
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                                                                                                                                                                                                                                61 adsvkgrftisrdnskntlylqmnslraedtavyycar-gwglrgeegdyymdvwgkgtm 119
                                                                                                                                                                                                                                                                 61 ADSVKGRFIVSRDNSRDIVELQMSSLRLEDTAVYYCATBGSFFGSIKGRYYLENWGQGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luman volunteers were immunised with hepatitis B vaccine. MD3-4, ZM1-1 and PEL1-1 hybridoma cell lines were derived from 12, ZM1-1 and PEL1-1 hybridoma cell lines were derived from 14 mbocytes of individuals immunised with Heptavax (Merck & Co). Antibodies PEL1-1, ZM1-1 and MD3-4, belong to the Iggl cids. The cell lines producing PEL1-1, ZM1-1 and ZM1-2 were deposited as AFC FM924, 9191 and 9192 respectively. The cell lines all behave as typical (mouse x human) x human hybridomas and produce their respective Abs in concs. ranging up to 25 mg/l in standard suspension culture. The heavy variable (VH) and light variable (LH) sequenced. Total RNA was extracted from 10(7) hybridoma cells
                                                                                                                                               l qvqlvqsqqqlvqpqqslrlscaasgftfssyamswvrqapqkqlewvaaisgsgqstyy 60
                                                                                                                                                                                      1 EVQLLESGGGVVQPGPSLPLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of each cell line. ss DNA was synthesised using AMV-reverse transcripterse and oligo-dT as primer. PCRS were performed and amplified DNA was size selected. ss DNA for sequencing was isolated from each positive clone after superinfection with MI3K07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of the VH region of monoclonal antibody PE1-1 against hepatitis B virus surgace antigen. Menatitis B virus; surface antigen; monoclonal antibody; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibodies active against Hepatitis B surface antigen - for diagnosis and treatment of Hepatitis B virus Example; Page 35, 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing was by the dideoxy chain termination method (Sanger
                                                               Length 140;
line can be improved by exectic monipolations
                                                                                                   Mismatches 17; Indels
                                                           Score 553; DB 23;
Pred. No 1.18e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     T 13
R54047 standard; Protein, 143 AA.
                                                                                                       50:
                                                           Query Match
Best Local Similarity 69 6%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-1994 (first entry)
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  tumeur cell line o
Sequence 140 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label- leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label- VH III
                                                                                                                                                                                                                                                                                                                                                         121 VTVSS 125
                                                                                                                                                                                                                                                                                                                120 vtvss 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label- CDR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label- CDR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JH 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               R54047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label
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70.7%; Score 651; DB 9; Length 143;

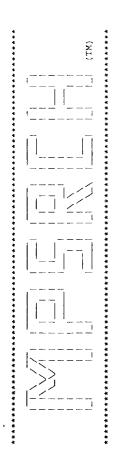
Query Match

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80 adsvkgrftisrdnskntlflgmhslraadtgvyycakdglyfgsgspghy----wvggtl 136
                                                                                                                                                                                                    61 ADSVKGRFIVSPRNSPDTVFLQMSSLRLEDTAVYYCATEGSPFGSIKGRYYLENWGQGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ADSVEGRIVSFONSFOTVFLQMSSIPLEDIAVYYCAFEGSPFGSIRGRYYLENWOLGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 evglvesgggvvgpgsslrlscaasgftfssfamhwvrqapgkglewvavmsysgdnkyy 50
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                                                                                                               1 EVQLLESGGGVVQPGRSLPLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDGSNQYY 60
                       3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SpA-reactive IgM heavy chain clone KIM.
SpA domain D; Ig binding region; IgM. B-cell superantigen, sAg,
superantigen; heavy chain variable region; VH3 restricted antibody;
VH; protein-A; KIM; B-lymphocyte; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SpA-reactive IgM heavy chain clone RIV.
SpA domain D; Ig binding region; IgM: B-cell superantigen; SAg;
Superantigen; heavy chain variable region; VH3 restricted antibody;
VH; protein-A; RIV; B-lymphocyte; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 Vdsvkgrftisrdnskntlylgmnslraedtalyycaklstaasgftfdtygmdwggttl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stimulating prodn. of variable region gene family restricted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIM is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 70.6%; Score 650; DB 9; Length 125; Best Local Similarity 68.8%; Pred. No. 2.07e-42; Matches 86; Conservative 20; Mismatches 19; Indels
Fred No 1 720-42,
10; Mismatches 19: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JI 15
R54789 standard; peptide; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                      R54788 standard; poptide: 125 AA.
  Pest Loral Similarity 74.2%,
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1994.
29-0CT-1993; U10555.
30-0CT-1992; US-969936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 AA;
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                                                                                                                                                                                                                                                    137 vtvt 140
                                                                                                                                                                                                                                                                                            121 VIVS 124
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WO9409818-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ADSVKGRFIVSRDIVSRDIVFLQMSSLRLEDIAVXYCATEGSPFGSIKGRYYLENWQQGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strive Manual Well Stricted Mariable region gene family restricted attibodies - through B-cell super-antigen vaccination antibodies - through B-cell super-antigen vaccination bisclosure: Page 71: 130pp: English.

A B-cell superantigen (8Ag) is a fragment of SpA D domain that specifically binds the Pab Portion of variable region restricted antibodies. The SAg is used to enhance production of VH, especially antibodies. The SAg is used to enhance production of VH, especially WH3, restricted Abs. During attempts to identify sAgs, as sequences (R54784-801) of H chains from Iq reactive with mod-SpA, and as and obtained from combinatorial libraries were determined. 19M protein RIV is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
70.6%; Score 650; DB 9; Length 125;
Best Local Similarity 68.8%; Pred. No. 2.07e-42;
Matches 86; Conservative 20; Mismatches 19; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: Tue Feb 24 07:10:46 1998 Job time: 35 secs.
                                    (REGC ) UNIV CALIFORNIA.
11-MAY-1994.
29-0CT-1993; U10555.
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                                                                                 Silverman GJ;
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Page 1



Pelease 2 1D John F. Collins, Riocomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Feb 24 07-06-43 1998, MasPar time E 41 Seconds 501-596 Million cell updates/sec Pun on

Tabular output not generated.

>US-08-844-215-3 (1-128) from USO8844215.pep 915 1 EVQLLEQSGAEVKRPGSSVK......NCYPGFFQOWGQGTLVTVSS 128 Description: Perfect Score:

Sequence:

Scoring table:

59021 scqs, 21210389 residues **PAM** 150 Gap 11 Searched:

Post-processing Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 40 966; Variance 67 504: scale 0 505

Statistics

# SUMMARIES

Score	0	Query Match	Length	DB	ID	Des	Description	u o	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
53 6	0		117	N	HV1A_HUMAN	IG	HEAVY		V-I RE	-
4 52	$\sim$		117	ሆ	HV1B_HUMAN	Ľ	HEAVY	CHAIN	PRECITA	ģ.
479 52.3	C4		117	u	HV1G_HUMAN	HG	HEAVY	CHAIN	PFECTR	7.490-87
Ŋ	ij		143	ហ	HV1C_HTIMAN	ğ	HEAVY	CHAIN F	PRECUP	1.120-84
5 4	47.5		114	S	HV00_MOUSE	IG	HEAVY	CHAIN V	/ REGI	2.890-76
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428 46.8			140	Ŋ	HV02_MOUSE	ij	HEAVY	CHAIN	PRECUR	1.37e-74
<b>*</b>			120	u)	HV03_MCUSE	SI	HEAVY	CHAIN A	V REGI	4 110-74
4	46.3		124	ın	HV1D_HUMAN	Ξ	HEAVY	CHAIN V	V-I RE	1.246-73
4			124	'n	HV1E_HUMAN	SI	HEAVY		V-I RE	2.140.73
414 45.2	•		122	Ŋ	HV3G_HUMAN	IG	HEAVY	CHAIN V	V-III	3.01e-71
402 43.9	٠		117	'n	HV14_MOUSE	$_{\rm IG}$	HEAVY	CHAIN F	ррестр	150-
400 43.7			1117	S	HV13_MOUSE	HG	HEAVY	CHAIN 1	V REGI	4.6
4			117	S	HV12_MOUSE	16	HEAVY	CHAIN V	V REGI	6 430-68
395 43.2	43.2		~~	S	HV51_MOUSE	IG	HEAVY	CHAIN V	V REGI	.87e-
394 43 1	43 1		$\vec{}$	ľ,	HV52_MOUSE	Ľ	HEAVY	CHAIN	PPECUR	- Ö Ü -
391 42.7			1117	u i	HV06_MOUSE	10	HEAVY	CHAIN	PRECUR	.75e-
4			117	r,	HV04_MOTISE	13	HEAVY	CHAIN	PPECUP	2.600-65
389 42 5	42 5		117		HV05_MOUSE	Ü	HEAVY	CHAIN	PRECUR	2.60e-65
₹			000		HV50_MOUSE	S	HEAVY	CHAIN V	V REGI	
			138	ሆነ	HV48_MCUSE	S	HEAVY	CHAIN	PPECUR	2.600-65
89 4	42 x		£.,	ď	HV07_MOUSE	5	HEAVY	CHAIN	PRECUR	2.600 65

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117 AA

STANDARD

RESULT 2 ID HV1B_HUMAN

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## ALIGNMENTS

HVIA_HUMAN STANDARD; PRT; 117 AA.  PULL 1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 21-JUL-1986 (REL. 01, LAST ANNOTATION UDDATE) 15 HRAVE GREEN OI, LAST ANNOTATION UDDATE) HOMO SAPIENS (HUMAN). 16 HRAVE GREEN OI (BU). 16 HRAVE GREEN REAGAS, CHOREATA; VEPTERRATA; TRIFAPODA; MAMMALIA; 17 HRATES. 17 HRATES. 18 FOUTHERIAS PRIMATES. 18 FOUTHERIAS A , PHTISHANSER H , GALL W E , GOTTLIEB P D., 19 MANDAL M.J. EDELMAN G.M.; 10 DISULEDDE BOND. MEDLINE; 71064027. 10 MEDLINE; 71064027. 11 HE SEQUENCE OF THE GAMMA-1 C PROTON OF THIS MYELOMA PROTEIN HAS BIOCHEMISTRY 9:3161-3176(1970). 11 HE SEQUENCE OF THE GAMMA-1 C PROTON OF THIS MYELOMA PROTEIN HAS ALSO BREN DETERMINED. 11 HE SEQUENCE OF THE GAMMA-1 C PROTON OF THIS MYELOMA PROTEIN WOLD PER ACCOSS: DIBBOI IPVB. 11 HAND OCCUPATION OF THIS MYELOMA PROTON OF THIS MYELOMA PROTEIN WOLD PER ACCOSS: DIBBOI IPVB. 11 HAND OF PER HIS HAS ACCOSS: DIBBOI IPVB. 12 96 14 FOUTH OF THE SEQUENCE OF THE MAMMA-1 THE SEQUENCE OF THE MAY PERSON OF THIS MYELOMA PERSON DESCRIPTION OF THIS MY PERSON DESCRIPTION OF THIS MYELOMA PERSON DE	Query Match Best Local Similarity 80 6%, Pred No. 7.61e-105; Matches 79, Conservative 10. Mismatches 8, Indels 1, Gaps	1 gyglv-gsgaeykkpgssykvsokasgglfsrsaliwyrgapgglowmgglypmfgppn 59 	60 yaqkiqqrvtitadestntaymelssirsedtafyfca 97 
HVIA_H HVIA_H 1017422 21-JU2. 21-JU2. 21-JU2. 21-JU2. 21-JU2. 31-JU2.	Query Match Best Local Matches		
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                                                                                                                                                                                                                                                                                                                                                                                                     20 qvqlv-qsgaevkkpgasvkvsckasgytfnsyymhwrqapgqglewmglinpsggsts 78
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                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG HEAVY CHAIN PRECURSOR V-1 REGION (V35).
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTERRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 88296408.
MATSODA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.O.ONO H., FUKUHARA S., HONJO T.:
FMRO J. 7:1047-1051(1988).
                                                                               METAZOA: CHORDATA; VEPTERRATA: TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION (V35).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 52.3%; Score 479; DB 5; Length 117; Best Local Similarity 70.7%, Pred. No. 7.49e-87; Matches 70; Conservative 11; Mismatches 17: Indels
                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION (HG3)
                                                                                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                        Query Match 52.9%; Score 484; DB 5; Length 117; Best Local Similarity 70.7%; Pred. No. 4.63e-88; Matches 70; Conservative 15; Mismatches 13; Indels
                                                                                                                                                       MEDLINE; 83144028.

RECHAVI G., RAM D., GLAZER L., ZAKUT P., GIVOL D.: PROC. NATL. ACAD. SCI. U.S.A. 80:855-859(1983).

EMBL; J00240, G553411; --

PIR: AC0204, HVHHG.

HSSP; P01810; 1FVB.

    79 yaqkfqgrvtstrdtsistaymelsrlrsddtvvyycar 117

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 yaqkfqgrvtmtrdtststvymelsslrsedtavyycar 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA; 13009 MW; FAA560D1 CRC32,
                                                                                                                                                                                                                                                                                                  117 117
117 AA; 12946 MW; BCC8BIDB CPC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
      21-01L-1986 (REL. 01, CREATED)
21-01L-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
10 HEAVY CHAIN PRECUPSOR V-I FEGION (HG3).
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO J. 7:1047-1051(1988).
EMBL, XO7448; -; NOT_ANNOTATED_CDS.
EMPL; SO0476; HVHU35.
HSSP: P01910; 1FVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMUNOGLOBULIN V REGION; SIGNAL
                                                                                                                                                                                                                                                  IMMUNOGLOBULIN V REGION: SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                        EUTHERIA; PRIMATES.
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 3
HV1G_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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CAPRA J.D., NISONOFF A.;
J. IMMINOL. 123:279-284(1979).
J. MMINOL. 123:279-284(1979).
SUBCLASS, THERE WAS NO HETEPOGENEITY IN THE HEAVY CHAIN V REGION SEQUENCE.
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE, 83055234.
KENTEN J.H., MOGGARD H.V., HOUGHTON M., DERRYSHIRE R.B., VINEY J.,
RELL L.O., GOULD H.J.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOIATION UPDATE)
IG HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
MUS MUSCULUS (MOUSE).
EUTHERIA; METADAA, CHORDATA, VERTEBRATA: TETPAPONA; MAMMALIA:
EUTHERIA; RODENTIA.
                                                                                                                                                               HOMO SAFIENS (HUMAN)
EUKRAYOTA; METAZOA; CHORDATA; VERTERRATA; TETKAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 470; DB 5; Leugth 143;
Pred. No. 1.12e-84;
23; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION (ND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID.
                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
61-NOV-1999 (PEL. 16. LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V-I REGION (ND) (FRAGMENTS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                         PROC. NATL. ACAD. SCI. U.S A 79.6661-6665(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T -> V (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 AA
                143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.48;
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nes 74; Conservative
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                      STANDARD;
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121
143
143 AA;
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LT 4
HV1C_HUMAN
P01744;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SAQKEQGRVSITADESASTAYMELSSLPSEDTALYYCAKDPPRECSGGNCYPGPPROCWOO 129
                                                                                                                                                                                                                                         1 evql-qqsgaelvkagssvkmsckatgytfssyelywvrqapgqgledlg-yissssayp 58
                                                                                                                                                                                                                                                                                      1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGGGLEWMGGSISFFGT-S 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 qvqlv-qsgaevkkpgssarlsckvsgddfntydihwvrqapgrglewmavvhpsddrtt 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTPSGHVTSWVPQAPGQGLEWMGGSISPFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (PEL 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V REGION (93G7).
MUS MUSCULUS (MOUSE).
EUKAPYOTA: METAZOA; CHORDATA; VERTERRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                            -,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
47.1%: Score 431, DB 5, Length 125,
Best Local Similarity 49.2%: Pred. No 2.62e-75.
Matches 63; Conservative 26; Mismatches 36; Indele
                                                                                                                                           Query Match
47.5%; Score 435; DB 5; Length 114
Best Local Similarity 67 0%; Pred No 2 89e-76;
Matches 71; Conservative 19, Mismatches 12, Indels
                                                                                                                                                Length 114
                                                                                                                                                                                                                                                                                                                                     59 nyaqkfqgrvtitadestntaymelsslrsedtavyfcavrvisry 104
                                                                                                                                                                                                                                                                                                                                                           PIR; A02022; GIMSAA.
HSSP; P01772; 1FGV.
IMMUNOGLOBULIN V PFGION: ANTIARSONATE ANTIRONY
                                                                        NON_IEP 114 114 SEQUENCE 114 AA; 12555 MW; 1A027FID CPC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 96 RY SIMILAPITY.
125 125
125 AA; 13579 WW; 67450023 CP032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
101-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-I REGION (MOT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D SEGMENT
J SEGMENT
RY SIMILAPITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AA
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KOJIMA M. KOIDE T., ODANI S., ONO T.;

MOL. IMMUNDL. 23.169-174(1986).

PIR; A02025; HVHUMO
HSSP: P01772; 8FAB.

IMMUNOSLOBULIN V PECTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V SEGMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
107
125
96
125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 qtllivss 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
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HV02_MOUSE
P01746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LI 6
HV1F_HUMAN
P06326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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EUP I IMMUNOL 12-1923-1032(1982).
EUP I IMMUNOL 12-1923-1032(1982).
EUP I IMMUNOL 12-1923-1032(1982).
EUP I ENDMA MAILYSIS OF THE SIZES OF SEVERAL OTHER DIFFERNITATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V PEGICNS HAVE PEAPPANGED TO THE SAME J SEGMENT, JH2.
FIRST V PEGICNS HANSCY
HSSP; P01789; 6FAB.
IMMUNOGLOBULIN V PEGION; ANTIAPSONATE ANTIBODY; HYBRIDOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 evgl-gqsgaclvragssvkmsckasgytftsyginwvkqrpggglewigyinpgngyin 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 vgl-gasgaelvragssvkmsckasgytftsyginwwkgrpggglewigyinpgngytky 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLLEQSSAEVKKPGSSVKVSCKASGGTFSGHVTSWVPQAPGGGLEWMGGSTSFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Saps
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                                                                                                                                                                                                                                                                                                                                                                                                       7; Gaps
STRAIN=A/J;
MEDLINE; 82152818.
SIMA,
SIMA I, PARBITTS T.H., ESTESS P , STAUGHTEP C , THOKEP P.W.,
CAPPA I D ;
SCIENCE 216.300-311(1902);
SCIENCE 216.3004;
SCIENCE 216.3009;
PERS. JOÓQUES, GASSOO7;
PERS. A02028; HVMSG7.
HSSP; POLTRO, FRAB
IMMUN-SLUBULIN V ESIGN, ANTIARSONATE ANTIECTY, HYBPHWMA, SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULUS (MOUSE).
EUKAPYOTA, METAZOA, CHORNATA, VERTERRATA, TETRAPODA, MAMMALLA;
EUTHERIA, RODENTIA.
                                                                                                                                                                                                                                                     IG HEAVY CHAIN V REGION (93G7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 120;
                                                                                                                                                                                                                                                                                                                                                     Score 428; DB 5; Length 140;
Pred. No. 1.37e-74,
27; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
46.5%; Score 426; DB 5; Length 120
Best Local Similarity 53.5%; Pred. No. 4.11e-74;
Matches 58; Conservative 29; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 83131846.
SIEKEVIIZ M., GEFTEP M.L., BPODEUP P., PIRLET P.,
                                                                                                                                                                                                                              1 19 15 HEAVY CHAIN V 140 140 MW. 07000508 CPC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 AA; 13307 MW; BBA8CCA1 CEC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SECTENCE UPDATE)
21-JUL-1986 (PFL. 01, LAST SECTENCE UPDATE)
1G HEAVY CHAIN V REGION (36-65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 AA
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54.7%;
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDAPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 gtpltvss 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECTENTE FROM N A
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                                                                                                                                                                                                                                                     CHAIN
NON_TEP
SEQUENCE
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SECTENCE
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PRT;
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                                                                                                                                                                                                               MEDLINE; 81013859.
LEHMAN D.W., PUTNAM F.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMPL: J00488: G554028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD
                                                                                                                                                                                                                                                                                      IMMUNOGLOBULIN V REGION.
                                                                                             STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
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HSSP; P01789; 11GI.
                                                                                                                                                                                                                                                                  PIR; A02051; M3HUAM.
HSSP; P01607; ZFGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 QGTLVTVSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 qgtlvtvss 122
                              114 qgvlvtvss 122
                                                    120 QGTLVTVSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HV14_MOUSE
P01758;
                                                                                             HV3G_HUMAN
P01768;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l qvqlm-qsgaevkkpgssvrvscktsggtfvdykglwvrqapgkglewvgqiplrfngev 59
                                                                                                                                                                                                                                                                                                    8, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANDREWS D.W., CAPRA J.D.:
BIOCHEMISTRY 20:5822-5830(1981).
-!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLUBULIN
                                                                                                                               ANDREWS D.W., CAPRA J.D.;
BIOCHEMISTRY 20:5822-5830(1981).
-i- THIS CHAIN WAS ISOLATED FROM AN 1GM WITH ANTI-GAMMA GLOBULIN
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                    IG HEAVY CHAIN V-I REGION (WOL).
IG SAPINS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

46.2%; Score 423; DB 5, Length 124;
Best Local Similarity 54.3%; Pred. No. 2.14e-73;
Matches 70; Conservative 23; Mismatches 28; Indels
                                                                                                                                                                                                                                                Score 424; DB 5; Length 124;
Pred. No. 1.24e-73;
20; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRECLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                          PYRROLIDONE CARBUXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AA; 13732 MW; C1E9663D CRC32;
                                                                                                                                                                                                                    124 124 AA; 13684 MW; 479BD3BE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
                         21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 124 AA.
      124 AA
      PPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V-I REGION (SIE).
                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 55.8%;
Matches 72, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, A02044; M1HUSI.
HSSP, P01857; 2FGW.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                          PIR; A02043; MIHUWL.
HSSP; P01607; 1FGV.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD,
       STANDAFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                               114 qgtlvtvss 122
                                                                                                                                                                                                                                                                                                                                                                                                   120 QGTLVTVSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82046599.
                                                                                                                          MEDLINE; 82046599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            HV1E_HUMAN
       HV1D_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                       NON_TER
SEQUENCE
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                                                                                                                SEQUENCE
                                                                                                                                                                                                             MOD_RES
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RESULT
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60 gvyikwe-rvivslkpsingaymelunlinedqavyycarew-k--qqvnvnp--idywq lll
                           l qvelve-sgggvvzpqrslxlscaasgftfsnyamhwvrqppgkqlewva-visybdbbk 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROC. NITL. ACAD. SCI U.S. A. 77.3239-3243(1980).
--- THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH
MACROSLOBULINEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŚEÓUENCE FROM N.A.
MEDILNE; B1245215.
ROIVOL D., ZAKUT R., EFFRON K., RECHAVI G., RAM D., COHEN J.H.:
KATURE 292:426-430(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
BUKARYOTA: METAZOA; CHORDATA; VERTEBRATA: TETRAPODA: MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHOKDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ж
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.2%; Score 414; DB 5, Longth 122; Best Local Similarity 49.5%; Pi=d No 3.01e-71; Matches 64; Conservative 30; Mismatches 27, Indels Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRROLIDONE CARROXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 117
117 AA, 12972 MW, 941G0G2E (90792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES 1 1 PYRROLIUNE CARROX
NON_TER 122 122 124 MV 4AF2E3.00 CPC*2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-30L-1986 (REL. 01, CREATED)
21-30L-1986 (REL. 01, IAST SEQUENCE HPDATE)
01-30L-1986 (REL. 34, LAST ANNOTATION UPDATE)
3G HEAVY CHAIN PPECUPSOP V PEGION (108A).
                                                                                                                                                                                                                                                                                                                21-UUL-1986 (REL. 01, CREATED)
21-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-UUL-1986 (PEL. 01, LAST ANNOTATION HPDATE)
11-GT HEAVY CHAIN V-111 KEGIÓN (CAM).
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA
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BY SIMILARITY.

96 117

DISULFID

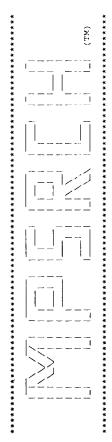
HSSP; P01772; 1FGV. IMMUNGELOBULIN V REGION; GLYCOPROTEIN.

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1 evql-gqsgpelvkpgasvkmsckasgytftdyymkwkqshgkslewigdinpnnggts 59
                                                                                                                                            20 evgl-ggsgpolvkpgasvkisckasgy+f+dynmhwykqshgkslow)gyiypynggtg 79
                                                                                                                                                                                                      1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVPQAPGQGLEWMGGSTSFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 400; DB 5; Length 117;
Pred. No. 6.43e-68;
23; Mismatches 21; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVPQAPGGGLEWMGGSISFFGTSN 60
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- THE SEQUENCES OF 10 HYPRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER PROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUP IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE: 83075344.
KEHRY M.R., PUHRMAN J.S., SCHILLING J.W., ROGERS J., SIBLEY C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV12_MOUSE STANDARD; PRT; 117 AA.
P01756;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V REGION (MOPC 104E).
MUS MUSCULUS (MOUSE).
EUKAPYOTA: METAZOA: CHOPDATA: VEPTERPATA: TETPAPODA: MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV13_MOUSE STANDAPD: PPT: 117 AA.
P01757;
21-JUL-1986 (FRL. 01, CFFATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NVV-1991 (REL. 20, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V REGION (J558).
MUSS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETPAPODA: MAMMALIA:
                                                                        ï
   Score 402; DB 5; Lenath 117
                                    Pred. No. 2.15e-69;
23; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCAKD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHILLING J., CLEVINGER R., DAVIE J.M., HOOD L.;
NATURE 283:35-40(1980)
                                                                                                                                                                                                                                                                          79 ynqkfkskatltvdnssstaymelssltsedsavyysar 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 ynqkfkgkatltvdkssstaymqlnsltsedsavyycard 99
                                                                                                                                                                                                                                                                                                                      61 SAQKFQGFVSITADESASTAYMELSSLFSEDTALYYCAK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 96 BY SIMILARITY.
117 117
117 AA; 13024 MW; E7548A05 CRC32;
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-!- THIS PROTEIN BINDS DEXTRAN.
PIR; A02039; MHMS4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE D AND J SEGMENTS.
--- THIS PROTEIN BINDS DEXTRAN.
PIR; A26242; MMSJ5
HSSP; P01789; 2F03M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.0%;
Matches 55; Conservative
Query Match
43.9%*
Best Local Similarity 55.5%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOGLOBULIN V PEGION.
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SEQUENCE
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Job time

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                                                                                                                                               Pred No 6 43e-68;
23; Mismatches 21; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Mismatches 21; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
MEDILINE: 84182519.
DILLEPOR F., PROVENS. V., SIEKEVITZ M., REYPENTHEP K., PAJEWSKY K., EMPO. V. 3:517-523(1984).
PIR, A02040; MHMS38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKAPYOTA: METAZOA: CHOBDATA: VEPTERPATA; TETPAPODA; MAMMALIA;
EUTHERIA: RODENTIA.
                                                                                                                        Query Match
43.7%; Score 400; DB 5; Length 117;
Best Local Similarity 55.0%; Pred No 6 43e-68;
Matches 55; Conservative 23; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 118;
                                                                                                                                                                                                                                                                                                                61 SAQKFQGPVSTTADESASTAYMELSSLPSEDTAIYYCAKD 100
                                                                                                                                                                                                                                                                             60 yngkfkgkatltrdkssstaymqlnsltsedsavyycard 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 395; DB 5; I
Pred. No. 9.87e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 ynqkfkgkatltvdksssatymelrsltsedsavyycar 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12934 MW; 2D1DCE77 CRC32;
                                                                                         1E0G0304 0E0555
                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (PEL. 06, CPEATED)
01-JAN-1988 (PEL. 06, LAST SEQUENCE UPDATE)
01-MAP-1992 (PEL. 21, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V PEGION (AC38 205 12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
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                                                                                         12992 XW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guery Match 43.2%;
Eest Local Similarity 53.5%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; PO1772; 1FGV.
IMMUNOGLOPULIN V REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
104
118
96
118
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22
118
118 AA;
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55
117
117 AA;
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HV51_MOUSE
P06330;
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NON_TER
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Release 2.10 John F. Collins, Biocomputing Pesearch Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Peb 24 07:07:23 1998; MasPar time 8.32 Seconds 468.769 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-844-215-3 (1-128) from USC8844215.pep 915 1 EVQLLEQSGAEVKRGSSVK.

Description: Perfect Score: Sednence.

NOYPGFFQQWGQGTLVTVSS 128

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir53 Database:

Tanni 2:ann2 3:ann3 4:ann4 5:unann1 5:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unann11 16:unann12 17:unenc 18:unrev

Mean 40.399; Variance 101.115; scale 0.400 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	08	QI	Description	Pred. No.
H	969	76.1	125	^	PH0957	heavy chain V	
C3	641		C.1	^	FH0952	Iq heavy chain V req	8
m	637		129	1	A33548	heavy chain V-	.12c-8
4	635	4.69	127	7	PH0955	heavy chain V	d
S	633	σ.	126	^	333548		50-8
9	625	œ	135	7	PH0953	heavy chain V	8.0
7	624	ω,	3	7	PH0954	heavy chain V	.44c
80	614	۲.	3	۲.	S46394	Iq heavy chain V req	2.32e-78
6	611	ø	æ	7	C33548	heavy chain V-	136-
10	611	9.99	627	7	S14683	Iq mu chain precurso	7.13e-78
11	610	66.7	7	7	PH0962	Ig heavy chain V reg	1.04e-77
12	609	9	$^{\circ}$	7	A49590	heavy chain V	7
13	605	66.1	4	7	S36261	heavy chain V	.75e-7
14	603	٠ ک	Н	7	PH0959	heavy chain V	.43e-7
15	601		122	۲۰	PH0958	Iq heavy chain V red	.02e-7
16	601	'n	3	7	PH0960	g heavy chain V	.02e-7
	598	'n	160	۲.	C	ti-PR2 erythroc	9.296-76
	594	64.9	86	^	S26915	q heavy chain	4.15e-75
19	594	4	116	7	831698	g heavy chain pr	4.15e-75
	294	64.9	119	۲.	S	heavy chain	4.15e-75

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4 15e-75 4 15e-75	.04e-7	.78e-7	696-7	.546-7	.04c-7	54e-7	.35e-6	27e-6	.84e-6	.61e-6	,15e-6	.15e-6	.71e-6	.23e-6	.36e-6	.06e-6	.02e-5	.52e-6	9-a/6	270-6	.6le-6	.57e-6	.086-6
Ig heavy chain V-n-I	g heavy chain V r	g heavy chain V1 r	y heavy chain V	g heavy chain V	g heavy chain V-	g heavy chain pr	q heavy chain Vl	g heavy chain V	g heavy chain	g heavy chain V	g heavy chain V-	g heavy chain V	q heavy chain V	g heavy chain V									
7 S44106 7 S44108	04050	82468	PH166	83626	D3354	52227	54646	C4959	GIHUE	84639	PH087	\$2192	PH166	53527	A3052	F4959	S1966	83166	8000S	PH167	A3248	83626	14415
119	1 (1	Œ١		$c_1$	C1	មា កា កៅ	$\mathbf{C}^{*}$	$\sim$	117	C1	$\sigma$	œ	108	€4	$\sigma$	$\vdash$	C4	Н	4	0	4	118	CI
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21	1 61	či	25	90	27	38	60	30	31	32	33	34	35	36	37	38	39	40	41	4.2	43	44	45

### ALIGNMENTS

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Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chronic
                                                                                                                                                                                                                                                                                                                                                             *superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#fitle Evidence for somatic selection of natural autoantibodies.
#cross'references MUID:92202880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 yaqkfqgrvtitadkststaymelsslrsedtavyycarqqnydyiwgsyrsndafdiwg 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGGGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapgqglewmggiipifgtan 59
       PH0952 *type fragment (G+ CLL-SMI) - human (fragment) | Jig heavy chain V region (G+ CLL-SMI) - human (fragment) #formal_name Homo sapiens #common_name man 17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A33548 *type complete
Igheavy chain V-1 region (NEI) - human
1#formal_name Homo sapiens *common_name man
1#formal_name Homo sapiens *common_name man
17-3an-1990 *sequence_revision 17-3an-1990 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carson, D.A.

Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917

Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in lymphocytic leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.1%; Score 641, DB 7, Length 128: 73.6%; Pred. No. 9.16e-83; ative 14; Mismatches 18, Indels 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                      #region framework 1\
#domain immunoglobulin homology #label IMM\
#region complementarity-determining 1\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #region complementarity-determining 1\
#region framework 2\
#region complementarity-determining 2\
#region framework 3\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #region complementarity-determining 3
#length 128 #checksum 3537
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                                                                                                                                                                                                                                                                                                                                                                                         heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -129 ##label KIP
                                                                                                                                                                                                                                                                                                                                           1-128 ## Label MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #cross-references MUID:89345575
#accession A33548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 73.6%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A33548; PH0956
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                                                                                                            16-Aug-1996
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*superfamily immunoglobulin V region; immunoglobulin homology
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#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic scientics of natural authorities.
#cross-references MUID:92202880
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69.6%; Score 637, DB 7, Longth 129;
Best Local Similarity 74.6%; Pred. No. 4.12e-82;
Matches 97; Conservative 14; Mismatches 16; Indels
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#title Developmentally restricted immunoqlobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
#cross-references MUID:89345575
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*formal_name Homo sapiens #common_name man
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J. Exp. Med. (1992) 175:983-991
Evidence for somatic selection of natural autoantibodies
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*superfamily immunoglebulin V region; immunoglobulin homology heterotetramer; immunoglobulin
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#journal J. Exp. Med. (1992) 175.983-991
#title Evidence for somatic selection of natural autoantihodies
#cross-references_MUID:92262880
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Query Match 68.3%; Score 625; DB 7: Length 135; Best Local Similarity 79.5%; Pred. No. 3.74e-80; Matches 89; Conservative 14; Mismatches 5; Indels
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Proc. Natl Acad. Sci U.S A (1989) 86:5913-5917
Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
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                                                                 ##cross-references EMBL:231681
FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
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#accession C33548
preliminary
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Proc. Natl Ac
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RESULT

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#superfamily immunoglobulin V region: immunoglobulin homolody
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#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural automntibodies.
#accession PH0962
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Nucleic Acids Res. (1990) 18:4278
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Pred. No. 7.13e-78;
12; Mismatches 16; Indels
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Pred. No. 1.04e-77;
12; Mismatches 10; Indels
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#cross-references MUID:90332450
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Matches 98; Conservative
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Local Similarity 73.9%;
tes 99; Conservative
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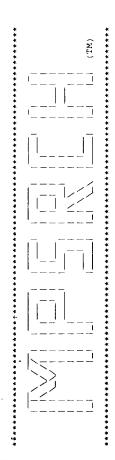
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Query Match
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##note sequence extracted from NCPI backbone
FICATION #superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                   A49590 #type fragment
Ig heavy chain v region (ACHSVI, clone 15) - human (fragment)
#formal_name Homo sapiens #common_name man
06-oct-1994 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffiths, A.D ; Malmqvist, M : Marks, J D : Pye, J.M ;
Embleton, M.J.: McCafferty, J : Raier, M.; Holliger, K P ;
Gorick, B.D : Hughes-Jones, N C : Hoogenhoom, H P.: Winter,
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Human anti-self antibodies with high specificity from phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary; not compared with conceptual translation
                                                                            60 yaqkfqqrvtitadosistaymelsslrsedtavyycarqqv···aq·r·-p-hfdywgq 112
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1 gvglv-gsgaevkkpgssvkvsckasgdt[ssyaiswvrqapggqlewmodiipifgtan 59
                                      1 EVOLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVR@AP@@@lewmaasisFFGTSN 60
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03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              #journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:355-359
#title Recombinant human Fab to glycoprotein D neutralizes infectivity and prevents cell to-cell transmission herpes simplex viruses 1 and 2 in vitro.
#cross-references MITD-04105168
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Ig heavy chain V region (clone alpha-TNF-E7) - human
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Pred. No. 1.516-77;
15; Mismatches 18, Indels
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##residues 1-121 ##label BUR
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Matches 87; Conservative
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#journal J Exp Mrd. (1942) 175-983-991
#title Evidence for americ selection of natural autoantibodies.
#cross-references MUID:92202880
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gvgl-gesgaevkkpgssvkvsckasggtfssyaiswvrgapggglewmggiipifgtan 59
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Ig heary chain V region (G6 *T.226) · human (fragment)
#formal_name Home sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 *text_change
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                                                preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                         #domain immunoglobulin homology #label IMM
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                                                                                                                                                                                                                                                                                                                                                                        6; Indels
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#region framework 3\
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display libraries.
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Best Local Similarity 82.5%;
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                                                                               ##molecule_type mRNA
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##status
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PH0952

REFERENCE

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#Journal J. Exp. Med. (1992) 175:983-991
#file Evidence for somatic selection of natural autoantibodies.
#file Evidence for somatic selection of natural autoantibodies.
##scession PH0958 MUID:92202880
##scession PH0959 DNA
##scatus nucleic acid sequence not shown
##sfatus nucleic acid sequence not shown
##sfatus nucleic acid sequence not shown
##sfatus nucleic acid sequence not shown
##scessions superfamily immunoglobulin homology #label IMM\
##scession ##scession complementarity-determining 1\/
##scession complementarity-determining 2\/
##scession framework 3\/
##scession complementarity-determining 3\/
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##scession complementarity 82.9% pred No. 3.02e 76.
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Pelease 2.15 John F. Collins, Biocomputing Research Unit. Copyright (c) 1994, 1994, 1995 University of Edinburgh, W.K Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07.35.05 1998; MasPar time 3 29 Seconds 198.618 Million cell updates/sec Pun on.

Tabular output not generated.

Title: Description: Perfect Score:

>US-08-844-215-3 (1-128) from US08844215.pep 915 Sequence:

PAM 150 Gap 11 Scoring table:

56402 seqs, 5095871 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

a-issued libackl 2:51 3 52 4 53 5 54 6 55 7:56 8 pcmq0 9-pcmq1 l0-pcmq2 11-pcm93 12:pcm94 13-pcm95 14-pcm94 Database:

Mean 28.046; Variance 135.560; scale 0.207 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred No.
- H	628	58.6	1 64	. 5	PCT-US95-0	Sequence 45, Applicati	3.50c-44
7	809	4 y	120	-	PCT-11593-1	13	1 930-42
3	909	66.2	120	11	PCT-US93-1	ci ri	2.886-42
4	585	63 9	147	Ç.	US-08-217-	4 . A	1.870-40
S.	560	61.2	102	0.1	PCT-US92-0	55,	2.68e-38
9	260	61.2	102	7	US-08-053-	63,	2 680.3B
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8	560	61.2	102	7	US-07-834-	۲,	C.
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13	553	60.4	117	9	US-08-477-	72	i
14	553	60.4	117	v.	-18-01-634-	۲,	1.080-37
15	553	60.4	117	Ç,	US-07-634-	4 , A	
16	553	60.4	117	ĸ	- PEY-10-SI	72	1.080-37
17	553	60.4		9	US-07-634-	10	H
18	553	60.4		9	80-	10	÷
19	553	ψ. Ūÿ		7	-13-08-481-	15, A	1.080-37
20	553	60.4		7	US-08-487-	72,	1.08e-37
21	553	60.4	117	7	US-08-474		1.080.1
22	553	£0.4	117	۲٠	US-08-474-	72, A	1.08c-37

11.088e. 12.088e. 13.74 + 4 + 4 + 4 + 1 + 1 + 1 + 1 + 1 + 1 +
Sequence 104, Application Sequence 104, Application Sequence 12, Application Sequence 12, Application Sequence 13, Application Sequence 11, Application Sequence 11, Application Sequence 12, Application Sequence 15, Application Sequence 155, Application
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## ALIGNMENTS

RESULT 1  DE PCT-US95-01219-45 STANDARD; PRT; 129 AA.  AX XXXXX  XX XXXXXX  10-JAN-1900  XX Sequence 45, Application PC/TUS9501219.  CC GRUEPAL INFORMATION:  APPLICANT: Agent of CTUS9501219  CC APPLICANT: Saldanha, Jose  CC APPLICANT: Abnesion Molecule VLA-4  NUMBER OF INVENTION: Adhesion Molecule VLA-4  CC COMPUTER: California  CC COMPUTER: CALIFORNIA:  CC COMPUTER: DATA APPLICATION  CC COMPUTER: PEARABLE FORM.  CC COMPUTER: TRAPERICATION:  CC COMPUTER: TRAPERICATION:  CC COMPUTER: TRAPERICATION:  CC COMPUTER: DATA:  CC COMPUTER: Saldanha, JOSE  CC COMPUTER: TRAPERICATION:  CC COMPUTER: TRAPERICATION:
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METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
                                                                                                                                                                                                      60 NYAOKFOGRVIITADTSTSTAYMELSSLRSEDIAVYYCARAPG-YGSGGGCYRGDYXFDY 118
                                                                                                                                                                                                                                  60 NSAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCAKDPPRFCSGGNCYPG-F-FQQ 117
                                                                                                                                                 1 QVQLV-QSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDT 59
                                                                                                                                                                           1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISF-FGTS 59
                                                                                                                       5; Gaps
                                                                                        Score 628, DB 13, Longth 129;
Pred. No. 3 60e-44;
15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-INDS/MS-INDS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JMREP PCT/US93/10555
29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application PC/TUS9310555 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application PC/TUS9310555.
                                        TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 129 AA; 13930 MW; 96169 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPAX: (619) 455-5110
INFORMATION FOR SEQ ID NO. 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Howells, Stacy L. REGISTPATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF INVENTION: THEREOF NUMBER OF SPOUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 amino acids
LENGIH: 129 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                           single
                                                                                                           Best Local Similarity 72.5%;
Matches 95; Conservative
                                                                                               68.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER .
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California
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               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25 CLASSIFICATION:
                                                                                                                                                                                                                                                                     119 WGQGTLVTVSS 129
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                         SIRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                  Query Match
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Sequence 12, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
ITILE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TILLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIHODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
                                                                                                                                                                           60 AQKEQGRVIIIADESINIAYMELRSLRSDDTAMYYCAKEG--Y---GD-YGRPFDFWGQS 113
                                                                                                                                                                                        Gaps
                                                                                                                                          1 VHLV-QSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFFGUANY 59
                                                                                                    15, Mismatches 11; Indels 7:
                                                                            Score 608; DB 11; Length 120;
Pred. No. 1.93e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Fatentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                      120 AA
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29-001-1993
                                                                                                                                                                                                                                                                                                      PRT;
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COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application PC/TUS9310555.
                                  NAME/KEY: Peptide
LOCATION: 1..120
ICE 120 AA; 13008 MW; 78865 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Howells, Stacy L. REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: THEREOF
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                                                                                                                                                                                                                                                                                                     STANDAPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 amino acids
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COPPESPONDENCE ADDRESS:
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                                                                                / Match 66.4%;
Local Similarity 74.0%;
nes 94; Conservative
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California
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STRANDEDNESS: sin
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IMMEDIATE SOURCE:
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PCT-US93-10555-12
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                                            SEQUENCE 120 A
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             CLONE:
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                       FEATURE
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                                                                                                                             Score 606; DR 11; Length 120;
Prod No 2 MMs-42;
15; Mismatches 10; Indels 7; Gaps
                                                                                           1 VQLV-QSGAEVKRPGSSVKVTCKASGDIFSSSAISWVPQAPGGGLEWMGGIIPIEGIPNY 59
                                                                                                             2 VQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSNS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 585. PP 6. Length 147;
No. 1 872-40;
                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend Khourie and Grew
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TBW PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1 0, Version #1 25
                                                                                                                                                                                                                                                                                   Sequence 4, Application US/U8217918
Patent No. 5506120
Patent No. 5506120
APPLICANT: LAKE, PHILIP
APPLICANT: CASTBERG, LARS
TITLE OF INVENTION: HUMAN ANTIRODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
                                                                                                                                                                                                                 147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
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DENCE 147 AA; 15801 MW; 123306 CN;
                                                                                                                                                                                                                PPT;
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Pred No 1
                        NAME/KEY: Peptide
LOCATION: 1..120
ICE 120 AA: 12984 MW; 80846 CN;
                                                                                                                                                                                                                                                                    Sequence 4, Application US/08217918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION NAME: Smith, Willaim M PEGISTRATION NUMBER 30, 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: (415) 325-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 325-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEC ID NO. 4 · SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                   STREET 374 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 amino acids
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APPLICATION NUMBER US,
                                                                                                                                                                                                                  STANDAPD;
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70.28.
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CORRESPONDENCE ADDRESS
                                                         Query Match
Best Local Similarity 74 #%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM.
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IMMEDIATE SOURCE:
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                                                                                                                                                              114 TLVTVSS 120
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         CLONE:
FEATURE:
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                                          SEQUENCE
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Local Similarity

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                                           20 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSNFATSWVRQAPGGGLEWMGRIMPLFVIST 78
                                                                                  1 EVOLLEGASAEVKKPSSSVKVSCKASGSIESGHVISWVRGAPGGGLEWMGGSISFFGISN 60
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larity 80.8%; Prod. No. 2.68e-38;
Conservative 11; Mismatches 7; Indels 1; Gaps
  92; Conservative 15; Mismatches 18; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
UMBBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One Market Flaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 YAQKEQGPUTITADPSISTAYMEISSLPSEDTAVYYGAP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCI/US92/06185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55, Application PC/TUS9206185 GENERAL INFORMATION:
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SEQUENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   William M. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/POCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE. 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION-
NAME: Smith, William M.
PEGISTPATION NUMBEP: 87654
                                                                                                                                                                                                                                                                                                                                                 STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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: California
RY: USA
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                    137 WGQGTTVTVSS 147
                                                                                                                                                                                                                                                             118 WGQGTLVTVSS 128
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tes 80; Conserv
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PCT-US92-06185-55
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RESULT
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                                            5 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIAN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                   APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for ITILE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 560; DB 7; Length 102; Pred. No. 2.68e-38; 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                            102 AA
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   61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCAK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIPRICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
APPLICATION NUMBER: US 07/853,408
APPLICATION DATA:
                                                             PRT
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                            Sequence 63, Application US/08053131 Patent No. 5661016 GENERAL INFORMATION:
                                                                                                                                                Sequence 63, Application US/08053131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX. 415-326-2422
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 102 amino acids
amino acid
                                                             STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.2%;
Best Local Similarity 80.8%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                         San Francisco
California
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                                                                                                                                                                                                                                                                                                                                                                                94105
                                                          US-08-053-131-63
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5 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSSYATSWVRQAPGQGLEWMGRITPILGIAN 63
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                                                                                                                                                                                                     APPLICANT: Lonberg, Nils
APPLICANT: KAPY, Robert M.
TILLE OF INVENTION: Transgenic Non-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                           ADDRESSEE: William M. Smith
STREET One Market Plaza, Steuart Tower, Suite 2000
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  102 AA.
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  PRT;
                                                                                                                                                            Sequence 63, Application PC/TUS9210983 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 55, Application US/07834539A
                                                                                                                      Sequence 63, Application PC/TUS9210983.
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JENCE 102 AA; 10940 MW; 55781 CN;
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
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TELECOMMUNICATION INFORMATION:
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  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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CITY: San Francisco
CTATE: California
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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GENERAL INFORMATION:
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PCT-US92-10983-63
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COMPULER READABLE FORM:
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TITLE OF INVENTION: Transgenic No. 553425-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
NIMBREP OF SECURENCES. 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSSYAISWVPQAPGGGLEWMGPIIPILGIAN 53
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GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TILLE OF INVENTION: HUMAN MONOCLONAL ANTIRODIES TO HERPES
TITLE OF INVENTION: SIMPLEX VIRUS AND METHODS THERFFOR NUMBER OF SEQUENCES: 25
CORPRESPONDENCE ADDRESS:
                                                  ADDRESSEE: William M. Smith STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 102
                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Polease #1.0, Version #1.25
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1880 Century Park East, Suite 500
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                                                                                                                                                                                        APPLICATION NUMBER: US/07/834,539A FILING DATE: 19920205
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                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
ENCE 102 AA: 10940 MW: 55781 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application PC/TUS9500067
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                        REPERENCE/DOCKET NUMBER 14
TELECHMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPRA: 415-543-5043
                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                            : 102 amino acids
AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                   single
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                                            CORRESPONDENCE ADDRESS:
                                                                                                                      COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RD 88.
Matches 80: Conservation
                                  NUMBER OF SECUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                 COUNTRY
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61 FQDRLTITABVSTSTAYMQLSGLTYEDTAMYYCAP-VA-YMLEPTVTAGGLDVWGQGTTV 118
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APPLICANT: CO. Man Sung
APPLICANT: CO. Man Sung
APPLICANT: SCHEIDER, William P.
APPLICANT: COELINGH, Kathloen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK: IMPPOVED HYMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Townsend and Townsend Khourie and Crew
                  OPERATING SYSTEM: PC-1008/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.9%; Pred. No. 5.93e-38;
Matches 83; Conservative 70; Miscatches 19;
                                                                           P31/11S95/00067
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                                                                                                                                                                                                FD-3229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..122
FCE 122 AA, 12999 XW, 86643 CN,
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Patent No. 5693761
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                                                                                                                                                                                                               LELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
TNPORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino.
                                                                                                            CLASSIFICATION:
ATTOPNEY/AGENT INFORMATION-
NAME: Halle, Pb D, Lisa A.
PRETETRATION NUMBER: 38,347
IBM PC compatible
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: FD
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                                                                                          04-JAN-1995
                                                      CURPENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-474-040-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94301
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                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 TVAS 122
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54

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Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                                                                                                                                                           HS 07/590,274
                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/08477728 Patent No. 5585089 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08477728.
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER. 118
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415) 326-2400
                                                                                                                                                                                                                                                                                       19-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         FILING DATE: 19-DEC-1
PRIOP APPLICATION DATA:
APPLICATION NUMBER: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 80.6%;
nes 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                      Palo Alto
California
                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-477-728-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                           COUNTRY:
                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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SCCXEXEX
       1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSRSALIWVRQAPGQGLEWMGGIVPMFGPPN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..117
OTHER INFORMATION: /note= "Eu heavy chain amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: OCHEN, CATY L.
APPLICANT: SCHNED, William P.
ARPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMINOGIOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553; DB 7, Length 117
No 1.08e-37;
         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Townsend and Townsend and Crew LLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCA 98
                                                                                                                                                                                                                                                                                                                                                                                                       11823-002600
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                                                                                                                                                                                                                                                      PATOR APPLICATION DATA
PATOR APPLICATION NUMBER: US
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATE: 05/290,975
PRIOR APPLICATION DATE: US
APPLICATION NUMBER: US
FILING DATE: 28-DEC-1988
ATORNEY/AEBNT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-00260
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2400
TELEFAX:
                                                                                             APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: sequence."
CE 117 AA; 12472 MW; 77871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08477728 Patent No. 5585089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 80.6%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                    FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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US-08-477-728-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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l; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1.117
OTHER INFORMATION: /note= "Variable region of the human OTHER INFORMATION: En antibody heavy chain."
NCE 117 AA: 12472 MW: 77871 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
SOFTWARE: Patentin Release #1.5, Version #1.25
CURRENT APPLICATION DATA-
APPLICATION NUMBER: US/08/477,728
FILING DATE: US-0.3UN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/634,278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA
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Pred. No. 1.08e-37;
10; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YAQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                        11827-002600
                                                                                                                                                                                                                   FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION UNMBER: HS U7/290,975
FILING DATE: 28-DEC-1988
FILING DATE: 18-DRATION:
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94111
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                                                                                                      ADDRESSEE:
                                                                                                                                     COUNTRY
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01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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  1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSPSAIIWVPQAPGQGLEWMGGIVPMFGPPN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLLEQSGAEVKKPGSSVXVSTKASGGTFSGHVISWVRQAFGGGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1 117
OTHER INFORMATION: /note= "Eu heavy chain aminn acid
OTHER INFORMATION: sequence "
NCE 117 AA; 12472 MW; 77871 CN;
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E
TILLE OF INVENTION: IMPROVED HUMANIZED IMMUNGLOBLINS
UNDER OF SEQUENCES: 113
COPPESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 553; DB 6; Length 117;
Pred. No. 1.080-37;
10; Mismatches 8; Indels
                                                                                           COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PatentIn Pelease #1 0, Version #1.25
                                                Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA
                                                     Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 YAQKFQGRVIITADESTNTAYMELSSLRSEDTAFYFCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCA 98
                                                                                                                                 CLASSIFICATION 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA
APPLICATION DATA
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/577
PPIOR
                                                                                                                                                                                                                                                                                     FESTATEMENT OF THE TOTAL TOTAL TOTAL TELECOMMUNICATION INFORMATION:
TELECHONE: (415, 326-2400
TELEPHONE: (415, 326-2422
INFORMATION FOR SEQ ID NO: 15.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                       : 117 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: Protein
                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                            60.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 80.6%.
                                                             CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                      94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 13
US-08-477-728-72
                                                ADDPESSEE:
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                                                                                                                                                                                                                                                                                                                                        LENGIH
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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1 @V@LV-GSGAEVKKPGSSVKVSCKASGGIESPSAIIWVPQAPGGGLEWMGGIVPMFGPPN 59
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                                                                                                              APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOSLOBLINS
COPPESPONDENCE: 113
COPPESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.4%; Score 553; UB 6; Length 117; Best Local Similarity 80.6%; Pred. No. 1.08e-37; Matches 79; Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWAPE: Patentin Pelease #1 0. Version #1.25
CUPPENT APPLICATION DATA.
APPLICATION NUMBER: US/08/477,728
                                                                                                                                                                                                                                                                     Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                       STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-SEP-1940
PRIOR APPLICATION DATA: APPLICATION DATA: TS 07/310 DEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 37/310,252
FILING DATE: 13-FER-1989
APPLICATION DATA:
APPLICATION NUMBER: US 37/290,975
FILING DATE: 28-DEC-1988
ATTONREY/ARDI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/477,728
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/634,278
FILING PARF: 19-DEC-1990
PRIOP APPLICATION DAM:
APPLICATION NUMBER: US 07/590,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPEPATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 117 AA; 12472 MW; 77871 CN;
                                           Seguence 72, Application US/08477728
Patent No. 5585089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M
PEGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823
TELEPOMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
Sequence 72, Application US/08477728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PPIOP APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                            GENERAL INFORMATION:
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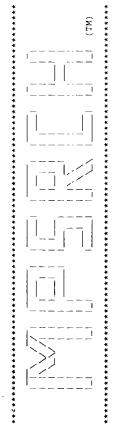
61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCA 98

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. 1 FVQLLEQSGAEVKRPGSSVKVSCKASGGTFSGHVLSWVRQAPGGSLEWM3GSISFFGTSN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /note= "Eu heavy chain amino acid
OTHER INFORMATION: sequence."
WCE 117 AA; 12472 MW; 77871 CN;
                                                                                                                                                             APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
ADDRESSPONNENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278 FILING DATE: 19-DEC-1990 CLASSIFICATION: 424
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Local Similarity 80.6%; Pred. No. 1.08e-37;
les 79; Conservative 10; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 11823-002600
TELECHONE. (415) 326-2400
TELEPHONE. (415) 326-2422
INFORMATION FOR SEQ ID NO. 15.
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
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APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
PEGISTPATION NUMBEP 30,223
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM in WEDIUM TYPE: Floppy disk COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                          Sequence 15, Application US/07634278
                                                                                                             CO, Man Sung
SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
                                  Sequence 15, Application US/07634278.
                                                                                                                                                                                                                ADDRESSEE: Townsend and TC
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                  QUEEN, Cary L.
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                                                                       GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICANT:
         01-JAN-1900
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En antibody heavy chain."
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                                                                                                                        APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COBLINGH Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNCGLOBLINS
NUMBER OF SEQUENCES: 113
COPPERSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 553; DB 6; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.08e-37;
10; Mismatches 8; Indels
                                                                                                                                                                                                                                Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: 19.06 FILING DATE: 19-DEC-1990 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Smith, William M
FEGISTATION NUMBER: 30,223
REFERENCE/POCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DE-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMPER: US 07/310,252
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                                                                                           Sequence 4, Application US/07634278 Patent No. 5530101 GENERAL INFORMATION:
                                                                         Sequence 4, Application US/07634278.
                                                                                                                                                                                                                                                                                                  COMPUTER READARLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEPAX: (415) 326-2422
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         379 Lytton Avenue
         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO FEATURE.
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Matches 79; Conservative
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: California
RY: US
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OTHER INFORMATION:
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JT 15
US-07-634-278-4
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Search completed: Tue Feb 24 07:35:16 1998 Job time : 11 secs.



Release 2 ID John F. Collins, Riccomputing Pescarch Unit, Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp | protein | protein database search, using Smith-Wainman algorithm

Run on: Tue Feb 24 07:08:10 1999; MasPar time 7.03 Seconds 252.969 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-3
Description: (1-128) from US38844215.pcp
Perfect Score: 915

Perfect Score: 915 Sequence: 1 EVQLLEQSGAEVKRPGSSVK...

NCYPGFFQQWGQGTLVIVSS 128

Scoring table: PAM 150 Gap 11 Searched 111726 segs, 19889129 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq30

liparti 2:part2 3.part3 4.part4 5.part5 6:part6 7:part7 9:part4 9:part8 9:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part23

Statistics - Mean 30 241; Variance 147 709; scale 0 205

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred, No.	5e-5	4.586-4	4.5	1.81e-4	7.139-4	a.	1.06e-3	1.28e-3	7 2.31e-3	6-491 #	5.06e-3	7.640.7	5 550-37	5.556-3	r 5.55e-37	0.00	1 1.216-35	2 136-3	2.182.36	98-469 : 0
Description	ednence of a	SpA-reactive IgM heav	Antibody D heavy cha	CEA-specific antibody	DF10 VH region.	CEA-specific antibody				93KA9 anti-Varicella	Anti-melanoma antibod	SpA-reactive 14M bear	HV1262 VH region.	Protein encoded by th	Human heavy chain V	ENA fragment vh49.8,	HSV-neutralising ant	Human antibody Eu hea	Heary thain variable	Messell callantitedy
OI	-	σ	P31023	W19888	R72068	W19RR7	W19881	W19889	WIGGE	R65019	W13536	F54795	ひょうごとは	R22358	R38623	OSOS OM	R75954	E24104	F28742	010015
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% Ouery Match	82.5		55.4	65.7	6.49	64.8	64.7	9.49	64.3	63.8	63.8	63.2	51.	61.2	61.2	61.2	60.8	60.4	#+ ('`)	6.23
Score	756	608	608	601	594	593	592	591	588	585	584	578	560	260	260	560	556	553	553	ਰ 6 6 6
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### ALIGNMENTS

SULT 1 R24442 standard; R24442 (fix C2-JAN-1992 (fix Sequence of antib Antibody; immunog Homo sapiens. Key Misc_difference 3 //note= "see above Misc_difference 3 /label= S /note= "see above Misc_difference 3 /label= S /note= "see above Misc_difference 3 /label= N Misc_difference 3 /label= N Misc_difference 3 /label= N	Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Miscalif Mis	
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61 SAQKFOGRVSITADESASTAYMELSSLRSEDTAIYYCAKDPPRFCSGGNCYPGFFQQWGQ 120
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                                                                                                                                                                                                                                                                                                                                                          84 yaqkiqgrvtitadeststaymelsslrsedtavyycardngaycsggscysqwfdpwgq 143
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additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding abulity. They are preferably located in the CH2 region of the Iq molecule. Antibodies bearing multiple sialyl-Lex determinants are useful for disrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury. Sequence 481 AA:
                                                                                                                                                                                                                                                                                                 25 qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtan 83
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                                                                                                                                                                                                                                    1; Gaps
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Spa domain D; Ig binding region: IgM; B-cell superantigen: sAg,
superantigen: heavy chain variable region: VH3 restricted antibody;
VH; protein-A; KAS; B-lymphocyte; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI: 94-167127/20.
Stimulating prodn. of variable region gene family restricted
antibodies - through B-cell super-antigen vaccination
bisclosure; Page 78: 130pp; English.
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Pred. No. 9.75e-54;
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larity 74.0%; Pred. No. 4.58e-41;
Conservative 15; Mismatches 11;
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R54796 standard; peptide; 120 AA.
                                                                                                                                                                                            Match 82.6%;
Local Similarity 81.3%;
Les 104; Conservative
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Matches 94; Conserv
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(HAV) sero positive patient. Antibody D is closely related in nature to murine antibody BSB3. Total RNA was isolated from antibody D expressing cells and polyademylated RNA was extracted. These polyA RNA's were used to prepare a cDNA library which was screened for human kappa light (L) chains and two positive clones were detected. Further heavy (H) chain clones were also isolated. Sequence 476 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 35pp; English.
The sequences given in R31023-24 represent the heavy and light chains of Antibody D respectively. Antibody D is a monoclonal antibody which was derived from peripheral blood lymphocytes from a hepatitis A virus (HAV) sero positive patient. Antibody D is closely related in nature
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70.3%: Pred. No. 4.58e-41;
ative 15; Mismatches 22; Indels 1; Gaps
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                                                                  Heavy, 11ght, chain, antibody: D: moncolonal portpheral blood;
lymphocyte, hepatitis A virus, HAV; sero; positive; patient;
murine: BSB3; polyadenylated; cDNA library; human; kappa; L: H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of recombinant primate antibodies - useful for treating
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                                                                                                                                    Location/Qualifiers
T
R31023 standard; Protein; 476 AA.
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                                            (first entry)
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                                                                                                                                                                                                                                                                                                            85..113
                                                                                                                                                                   "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991; GB-016594.
                                                         Antibody D heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1992; GB-006284
                                                                                                                                                                                                                                                                             69..84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= HINGE
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                                                                                                                                                                                                                                'label= CDR1
                                          19-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                    label= CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CH2
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                                                                                                                                                                                                  /label= FR1
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                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide sequence comprises the heavy chain variable region (YR), HBBI, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCBA) specific antibody CEA6 (see W19881). A claimed specific binding member (A) comprises an hCBA specific antibody antigen binding domain that has a dissociation constant for hCBA of lass than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 cextracellular domain of hCBA and/or to cell-associated hCBA over hCBA over soluble hCBA. Preferred (A) include pairings of VH and VL variants (see W19886-95) obtained by a swell as CBA6 VH and VL variants (see W19886-95) obtained by comparenesis or chain shuffling. An example of a claimed pairing is HBBI1 VH with CEA6 VU. (A) is used to detect cells expressing hCBA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 yaqkfqqrltitadeststaymelsslrsedtavyycarhnhny--elyyy--ymdvwqq 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLIEGSGAEVKKPGSSVKVSCKASGGIFSGHVISWVRQAPGQGSLEWMGGSISFFGISN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ľ.
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Pred. No. 1.81e-40;
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                                                                                                                                                                                       07-DEC-1997 (first entry)
CEA-specific antibody CEA6 VH mutant HBB11 sequence.
Carcinoembryonic antigen; CEA; human; antibody; scrv;
tumour marker; lung cancer; breast cancer; colon cancer;
adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhote= "complementarity determining region 1"
8egion
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-0CT-1996, GB-021295.
23-MAY-1996, GB-02004
23-MAY-1996, GB-010P24
(CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                       W19888 standard; Protein; 123 AA.
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Best Local Similarity 71.1%;
Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                          Chimeric Homo sapiens;
Chimeric synthetic.
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               121 GTLVTVSS 128
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1 gvglv-gsgacvkkpgssvkvsckasggtfssyaiswvrgapggglewmggiipifgtan 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin tissue and clones encoding autoimmune-associated immunoglobulin showed and prize the property of the closest germline genes, PP10 (20022) and hells? (200328) The DNA (200429) and corresp amino acid (P72770) sequences of the VH region of a representative clone, sequence 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Graves' ophthalmopathy-associated monoclonal antibody - produced
by molecular cloning of immunoglobulin genes by PCR
Disclosure; Page 68; 94pp; English.
                                                                         Graves ophthalmopathy associated immunoglobulin protein: orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scare 594, (4 12) (angth 98)
Pred. No. 7.13e-40;
10; Mismatches 4; Indels
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Carcinoembryonic antigen; CEA; human; antibody; scFv;
tumour marker; lung cancer; breas! cancer; color cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 yaqkfqgrvtitadeststaymelsslrsedtavyycar 98
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Region
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                                                                                                                                                                                                                                     /dabel_CDR2
W0950836-A.
30-MAR-1994: U10756.
22-SEP-1994: U10756.
(MIGH-) NICHOLS INST DIAGNOSTICS.
McHachlan SM, Rapoport B;
WPI; 95-139383/18.
                                                                                                                                                             Location/Qualifiers
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R72068 standard; Protein; 98 AA
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Best Local Similarity 84.8%;
Matches 84; Conservative
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                                    26-SEP-1995 (first entry)
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11-OCT-1996, GB-021295.
07-DEC-1995, GB-025004.
23-MAY-1996, GB-010824.
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                                                          DP10 VH region
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                                                                                                                                            Homo sapiens.
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                 R72068
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This polypeptide sequence comprises the heavy chain variable region (WH), HBAIL, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCBA)-specific antibody CER6 (see W19881). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 - 8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 to with human liver cells, and preferentially binds to the A3-B3 to CEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA17 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. (A) is used to detect cells contagned cancer, e.g. adendrationma of the rolon, lung or breact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 yaqkfqgr1titadeststayme1ss1rsedtavyyca-gans-cnrsyyy--ymdvrgq 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 14; Indels 5; Gaps
             WPI: 97-319779/29.
Specific binding members for human carcinoembryonic antigen - bind
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                                                    to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 593; DB 23; Length 123; Pred. No. 8.68e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEA-specific antibody CEÁ6 VH sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity determining region 3"
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89..112
Osbourn JK;
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                                                                                                          Claim 4; Fig 2; 128pp; English.
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Matches 91; Conservative
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McCafferty JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenocarcinoma; diagnosis.
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WPI: 97-319779/29.
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07-DEC-1995; GB-025004.
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           97-319779/29.
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12-JUN-1997.
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                                                                                           cancer
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60 yaqkiqqrltitadoststaymolselrsodtavyyoaqrshay--olyyy--ymdvwqq 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLLEQSGAEVKKPGSSVKVSGKASGGTFSGHVISWVFQAPQGG FWMGGSISFGTFSN FO
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                                                                                                                                                           A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding dowain that has a dissociation constant for hCEA of less than 1 x 10 - 8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to reil-associated hCEA over hCEA and/or to reil-associated hCEA over hCEA sequences from CEA1-7, or their CEP sequences, as well as CEA. WH and VL variants, including combinations of CEAB VH with VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide sequence comprises the heavy chain variable region (VH), HBB6, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (ACEA)-specific antibody CEA6 (see
                                                                                                                                                                                                                                                                                                                                                                                              regions from CEA6, Tofot, Tofo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Specific binding members for human carcingembryonic antiquen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
Claim 4; Fig la; 128pp; English.
This polypeptide sequence comprises the heavy chain variable region (VH) of human carcinoembryonic antique (hCEA)-specific antibody CEA6. WH 772125-25, and VL (T72138-55) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see W19876-85).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carcincembryonic antigen; CEA; human; antibedy; scFv;
tumour marker; lung cancer; breast cancer; colon cuncer;
adenocarcinoma; diagnosis.
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CEA-specific antibody CEA6 VH mutant HBB6 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 592; DB 23;
Pred No 106e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity determining region 1"
Region 50..66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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W19889 standard; Frotein; 123 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     no. lung or breast.
123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.78;
71.18;
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les 91; Conservative
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Specific antibody antigen binding member (A) comprises an hCFA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferred 10 -8 M, is non-cross-reactive with human liver cells, and preferred 10 -8 M, is non-cross-reactive with human liver cells, and preferred 10 -8 M, is non-cross-reactive cells and preferred (A) include pairings of VH and CML and VL well as soluble hCEA. Preferred (A) include pairings of VH and VL wariants (see W19876-55) obtained by mutagenesis or chain shuffling. An example of a claimed pairing is HBBS VH with CEAS VL. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tymour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 yaqkfqgrltitadeststaymelsslrsedtavyycaqrshty--elyyy--ymdvwqq 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 qvqlv-qsgaevkkpgssvkvsckasgqtfsnspinwlrqapqqglewmqsiipsfqtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secre 591, DR 23, Imegith 123, Pred, No. 1,286+39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 16; Indels
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Pegion
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(CAMB-) CAMBRINGE ANTIRODY TECHNOLOGY
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Best Local Similarity 71.1%;
Matches 91; Conservative
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07-DEC-1997 (first_entry)
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                                                                                                                                                                                                                                                                                                                                             61 SACKFOGRVSITADESASTAYMELSSLRSEDTALYYCAKDPPRCSGGNCYPGFFQQWGQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 claim 8; Fig 4B; 39pp; English.
A human anti-Varicocalla coster virus monoclonal antibody was prepd.
using the trioma method of Ostberg et al. (1983) Hybridoma 2:351-357.
One resultant trioma neutralised VZV in the absence of complement.
This call line, designated cell line TG93RAP, produced an antibody genes cell line, designated 93RA9 cpNA, for the light and heavy chain variable region heavy chain (gamma-1) and two light chain (kappa) specific clones sequence 147 AA;
                                                                                                                                                                                                                                        1 gygly-gsgaevkkpgssykysckasggtfsnspinwlrgapggglowmgslipsfgtan 59
                                                                                                                                                                                                                                                                          1 EVELLEGESTABVKKPERSSVKVSEFASSETFSGHVISWVPGAPGET EWMGGSISFEGISN | 60
                                                                                                                                                                                                   5, Gaps
hoPA over soluble hCBA Preferred (A) include pairings of VH and VI sequences from CBA1-7 (see W19976-85) or their CDP sequences. as well as CBA VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. Examples of claimed pairings are lifetio VH with locklic or CBA5 VL. (A) is used to detect ceils expressing hCBA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g adenorarinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Varicella zuster virus, VZW; anti-VZW monoclonal antibody, 93KA9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93KA9 anti-Varicella costor virus antihody heavy chain variable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human monoclonal antibodies specific for the glyco:protein II
                                                                                                                                                               Score 588; DB 23; Length 123;
Pred No 2 31e-39;
16, Mismatches 16; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   · used in a therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.9%; Score 585; DB 12; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- complementarity determining region (CDR)
Region 69..85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 150-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key Location/Qualifiers
Protein 20 147
/label= mature light chain
Pegion 50 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subjunit of varicella goster virus prophylaxis of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .r 10
R65019 standard; Protein; 147 AA.
R65019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprotein II subunit; vaccine
                                                                                                                                                               Match
Local Similarity 71 1%;
les 91, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 70.2%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SANO ) SANDOZ PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-1995.
22-JUL-1994; U08241.
28-JUL-1993; US-098479.
24-MAR-1994; US-217918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ostberg L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lake P, Ostberg L;
WPI; 95-090612/12.
N-PSDB; 282750.
                                                                                                                                                                                                                                                                                                                                                                                      116 gtmvtvss 123
                                                                                                                                                                                                                                                                                                                                                                                                                        121 GTLVTVSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region.
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                                                                                                                                                                                                     Matches
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2

Mismatches 18; Indels 6; Gaps

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20 qvqlv-qsgaevkkpqssvkvsckasgqtfsnfaiswvrqapgqglewmgrimplfvtst 78

qq

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same type as the patient's tumour; (c) removing extraneous antibodies by absorption against normal human cells; (d) cloning the phage selected in step (b) and (c); (e) assaying the specificity of the cioned phage by incubating the phage with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phage that do not bind to either cell line of cultured normal cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to cultured tumour cells derived from more than one other tumour that is not the patient's tumour. The present sequence represents a human heavy chain antibody, from a VH antibody fusion phage library, produced by a method as described above. The antibodies produced can be used for diagnostic and therapeulic applications and for isolating tumour antigens for studying tumourigenesis or for use as anti-cancer vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 19; Page 75-76; 82pp; English.

A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphocytes (PBLS) of a cancer patient; (b) screening for anti-tumour antibodies in the phage library in a binding assay with cultured tumour cells of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MAbs). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 rvtitadkststaymelsslrsedtavyyca····r··gggr·ydaf·diwgggtlvtvs 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 RVSITADESASTAYMELSSLRSEDTAIYYCAKDPPRFCSGGNCYPGFFQQWGQGTLVTVS 127
                                                                       61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCAKDPPRFCSGGNCYF-GFF-QO-117
                                                79 yaqkfqgrvtisadaststaymelsslrsddtamyycardita--pgaaptplnfygmdv 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 gglevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtanyaqkfgg 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 SGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSNSAQKFQG 67
1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAFGQGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                         28-OCT-1997 (first entry)
Anti-melanoma antibody 2-71 from VH antibody fusion phage library.
Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodn. of human monoclonal anti-tumour antibodies - by screening fusion phage library produced using peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour cell line can be improved by genetic manipulations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 584; DB 23; L
Pred. No. 5.06e-39;
11; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                              tumourigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R54795 standard, peptide, 120 AA. R54795;
                                                                                                                                                                                                                                                                      T 11 W13536 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 76.9%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JAN 1997.
28-JUN-1996; IB1032.
30-JUN-1995; US-497647.
(UYXA.) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from a cancer patient
                                                                                                                                                 137 wgggttvtvss 147
                                                                                                                                                                                                  118 WGQGTLVTVSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 97-109061/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 s 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 S 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                       W13536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                           qq
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60 aqlfqqavtittdeststaymevsslrsedtalyycareqrrm-ai-n--p--fdywqqq 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stimulating produ. of variable region wene family restricted antibodies - through B-cell super-antigen vaccination bisclosure; Page 77: 130pp: English.
A B-cell superantigen (sAg) is a fragment of SpA D domain that specifically binds the Fab portion of Variable region restricted antibodies. The sAg is used to enhance production of VH, especially VH3, restricted Abs. During attempts to identify sAgs, as sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l vglv-gsgaevkkpgssvkvtckasgdtfsssaiswvrqapqeqlewmquiipifqtpny 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VQLLEQSGAEVKKPGSSVKVSCPASCGTPSCHVISWVPQAPGOGLEWMGGSISPFGTSNS 61
                                                                                                                                                                                                                                                                                                                                       (R54784-801) of H chains from Ig reactive with mod-SpA, and as and DNA sequences (R54802-16, Q54842-56) of VH regions of SpA binders obtained from combinatorial libraries were determined. IgM protein BOR is derived from the germline configuration of a VH quee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Gaps
              Spa-reactive igm heavy chain clone BOR.
Spa domain D: Iq binding region: Iqwi B-cell superantiqen; SAU;
superantigen; heavy chain variable region; VH3 restricted antibody:
VH; protein-A: BOR: B-lymphocyte; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graves' ophthalmopathy-associated monoclonal antibody produced by molecular cloning of immunoglobulin genes by PCR Disclosure; Page 69: 94pp; English.

Lisang Hochain DNA was amplified by PCP from Graves' orbital tissue and clones encoding autoimmuno-associated immunoglobulin fragments were obtained 12715 clones of Hichain (1961) genes showed homology to the closest germline genes, 1999 (984)27) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV1263 VH region.
Graves ophthalmopathy associated immunoglobulin protein;
orbital antigen; monoclonal antibody, heavy chain; H chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 578; DB 9; 1
Pred, No. 1.64e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NICH-) NICHOLS INST DIAGNOSTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R72069 standard; Protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.28;
72.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Overy Match
Best Local Similarity 72.4%,
best Local 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rapoport B;
(first entry)
                                                                                                                                                     30-0CT-1992; US-969936.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-124469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31..35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-1994; U10756
                                                                                                                                        29-OCT-1993; U10555
                                                                                                                                                                                                        WFI, 94-167127/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI: 95-139383/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 tlvtvss 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 TLVTVSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q89328
                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mclachlan SM,
                                                                                                                                                                                           Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEF-1993;
                                                                                                                      11-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09508336-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-1995
 18-00T-T094
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                   sedment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R72069;
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1 qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmgriipilgian 59
                                                                                                                                                                                                               1 EVQLLEÇSGAEVKKPGSSVKVSCKASGGIFSGHVISWVRQAPGQGLEWMGGSISFFGISN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 gvglv-qsgaevkkpgssvkvsckasgqtfssyaiswvrqapgqglewmgrlipilgian 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.P.D.S. 022419.
Immunoglobulin trans:genes - for prodn. of heterologous Inmunoglobulin trans:genes - for prodn. of heterologous non-rearranged and/or rearranged ig chains
Example 14; Page 87; 172pp; English.
The human placental genomic DNA library cloned into the phage vector lambda FIX II was screened with the human VH1 family specific oligonoucleotide (see 022418). Phage clone lambda 49.8 was isolated and a 6.1 kb XbaI fragment cong. the variable segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8.
An 800 bp region of this insert was sequenced. VH49.8 was found to have an open reading frame which encoded the sequence shown.
(R72070) (Q89328). The DNA (Q89329) and corresp amino acid (R72070) sequences of the VH region of a representative clone, OP7H1.2, are provided. Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1992 (first entry)
Protein encoded by the human heavy chain V region gene VH49.8.
Heavy chain; variable region; VH1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 560; DB 4; Length 117;
Pred. No. 5.55e-37;
11; Mismatches 7; Indels
                                                                                                chain; minilocus transgene; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 yaqkfqgrvtitadkststaymelsslrsedtavyycar 117
                                                                                                                                                                                                                                                       60 yaqkfqgrvtitadkststaymelsslrsedtavyyrar 98
                                                                                                                                                                                                                                                                          61 SAQKFQGRVSITADESASTAYMELSSLRSEDTALYYÇAK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCAK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1993 (first entry)
Human heavy chain v region VH49.8.
Humunoglobulin; IGG, heavy chain; isotype switching; H chain variable
                                                                                                                                                                                                                                                                                                                                                           R22358 standard; Frotein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R38623 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.8%;
Matches 80; Conservative
                                                                                                                / Match
Local Similarity 80.8%;
Les 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENP-) GENPHARM INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-810279.
US-853408.
US-904068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-1991; U06185.
29-AUG-1990; US-574748
31-AUG-1990; US-575962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 92-113962/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lonberg N, Kay R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1991; 18-MAR-1992; 123-JUN-1992; 1
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WO9203918-A.
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has (GENP-) GENHARPM INT INC.

RAY RW. Lonberg N:

DR WPI: 93-214159/26.

DR N-PSDB: Q44185.

PTransgenic non-human animals contg. immunoglobulin heavy chain

PT Transgenic non-human placement of a non-fired into the phage vector

A human placental genomic DNA library cloned into the phage vector

CC A human placental genomic DNA library cloned into the phage vector

CC almoda FIX II was screened with the human VHI family specific

CC almoda FIX II was screened with the human VHI family specific

CC almoda fragment containing the variable segment VH49.8 was

CC cubcloned into pNNO3 to generate plasmid pVH49.8. An 800bp

CC region of this insert was sequenced (Q44185) and VH49.8 found to

Signals, indicating that the gene is functional. Amino acid

Signals, indicating that the gene is functional. Amino acid

CC codons before the termination codon have not been translated.

S Sequence II7 AA;
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Ouery Match 61.2%, Score 560, DB 7; Length 117, Best Local Similarity 80.8%; Pred. No. 5.55e-37; Matches 80; Conservative 11; Mismatches 7; Indels 1; Gaps

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Qy 1 EVQLLEQSGAEVKKP3SSVKVSGKASGTFSGHVISWVPQAPARH EWMANSISFFATSN 60 Db 79 yaqkfqarvtitadkststavmolss]rsodtavvvcar 117

20 gygly-gsgaevkkpgssykvsckasggtfssyaiswyrgapggglowmgriipilgian 78

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Search completed: Tac Feb 24 07:08:47 1998 Job time : 37 secs.

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Pelease 2 10 John F Collins, Riocomputing Poscarch Unit. Copyright (c) 1994, 1994, 1995 University of Edinburgh, T K Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tup Pab 24 07-04-15 1048; MasPar time 5 78 Seconds 465.989 Million cell updates/sec Tabular cutput not generated. Pun on:

....HIMGYYFDYWGQGTLVTVSS 127 (1-127) from US08844215.pep 931 1 EVQI-LEQSGAEVKKPGSSVK. >US-08-844-215-2 Description: Perfect Score: sedneuce.

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot34 Database:

l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11

Mean 42 278; Variance 75.769; scale 0.558 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred, No	2.65e-9 1.10e-8		8.24e-7	6.31e-7	ا ب	-906.4 4.90e-	III 4.90e	I RE 4.90e-	SCMP 1 340-	ECUP 2 22e-	226-5	RECTIP 3 66e-	1 000-6	7	4.52e-5	1 460-6	17.
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### ALIGNMENTS

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DISULFIDE BOND.
MEDLINE: 7104027.
GALL W.E., EDELMAN G.M.;
BITCHEMISTRY 9-3196(1970).
--- THE SEQUENCE OF THE GAMMA-1 C PEGION OF THIS MYELOWA PROTEIN HAS ALSO REEN DETERMINED
                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                          21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-I REGION (EU).
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHOPDATA: VERTEBRATA: TETRAPODA: MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.3%; Score 543; DB 5; Length 117; Best Local Similarity 76.5%; Pred. No. 2.65e-93; Matches 75; Conservative 11; Mismatches 11; Indels
                                                                                                                           SEQUENCE.
MEDLINE: 71064024.
MEDLINE: 71064024.
CUNNINGHAM R.A., FUTTSHAUSEP H., GALL W.E., GOTTLIER P.D.
WAXDAL M.J., EDELMAN G.M.;
FIGCHEMISTRY 9:3161-3170(1970).
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117 117
137 AA; 12472 MW; FGP9E175 CPC32;
          117 AA
          PRT;
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HSSP; P01810; 1FVB.
IMMUNOGLOBULIN V REGION.
          STANDARD;
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117
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        11-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-GT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HOROGONE CHAIN PRECURSOR V-I REGION (HG3)
HOMO SAPIENS (HIMAN)
EUKRAYOTA, METAZOA; CHOPCHAIA; VEFTERRATA; TETPAPUDA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE: 88296408.
MATSLINE: BESTALL NAKAI S., SATO T., KODAIRA M., ZONG S.Q., OHNO H. FUKTHARA S., HONJO T., EMBO J., 7:1047-1051(1988).
                                                                                                                                                                                                                                                                                                                                                               13: Mismatches 16; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHOPDATA: VEPTERPATA; TETPAPODA: MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                  Score 491; DB 5; Length 117; Pred. No. 1.10e-81;
                                                                                                                              SEQUENCE FROM N A MEDIINE, RIL4028.
MEDIINE, RIL44028.
FECHAVI G., RAM D., GLAZER L., ZAKUT R., GIVOL D.: PROC. NATL. ACAB. SCI. U.S. A. 80.855-R59(1983).
EMBL. JO0240: G553411;
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117 AA: 12945 MW: ECCEBIDE CRC32;
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01-NOY-1991 (PEL. 20, LAST SEQUENCE UPDATE)
01-NOY-1991 (REEL. 20, LAST ANNOTATION UPDATE)
101-NOY CHAIN PRECURSOR V-I REGION (V35).
HOMO SAPIENS (HUMAN).
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PIR: S00476; HVHU35.
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HSSP: P01810; 1FVB
IMMUNGLORULIN V PEGION; SIGNAL
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IMMUNOGLÖRMILIN V PEGTÖN; SIGNAL.
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Sest Local Similarity 59.7%;
Matches 69; Conservative
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Match 50.2%; Score 467; DB 5; Length 12%; Local Similarity 56.3%; Pred. No. 2.33e-76; ms 71; Cusservative 27. Mismutches 29. indebs 6; daps
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MARSHAK- POTHSTEIN A.,
EGF T. CAMTUNI. 12-1923-1932(1982).
FURL FROM AMAYSIS OF THE SIZES OF SEVERAL OTHER DIFFERNITATED GENES
THAT HYBRIDIZE TO THIS ONE. THE AUTHORS CONCLUDE THAT ALL OF
THESE V PEGIONS HAVE PEAPPANCED TO THE SAME I SEMBENT 142.
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                                                                             IG HEAVY CHAIN V PEGION (36-65).
MUS MUSCULUS (MOUSE).
EUKAKYOIA: METAZOA: CHOKDATA; VERTEBRATA: TETRAPODA: MAMMALIA:
EUTHERIA: PODENTIA:
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EUKARYOTA: METAZOA: CHOKDAIA: VERTEBRATA; TETRAPODA; MAMMALIA;
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125 125
125 AA: 13579 MW: 6245C023 CRC32;
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01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-I REGION (MOT).
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BY SIMILARITY.
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MOL. IMMUNDL. 23:169-174(1986).
PIR; A02025; HVHUMO.
ISSE, F01772, 8FAB.
IMMUNGCLOBULIN V REGION.
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HSSP; P01789; 6FAB.
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21-101-1986 (PEL
21-10L-1986 (PEL
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HV1F_HUMAN
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ID HV03_MOUSE
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                           P01747;
                                                                                                                                                                                                                                                                                                           NON_TER
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SIGNAL
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                     60 ygprsqarftvtrdsstttvymeltalisadtalyycarga-hysdtddsgtslgpwggg 118
                                    74 nyapríggrvtmtrdasfstaymdlrslrsddsavfycaksdpfwsdyynfdysytldvw 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 NYAOKFOGPLSTTAPDSTSTAYMELSSLPSEDTAVYFCAPV-VI-PNAIRHTMGYYFDYW 117
1 EVOLLEOSGAEVKKPGSSVKVSCQVFGDTFSFTTIQWLFQAPGGGPFWMGNTFPVYNTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 qtqlv-qsgaevrkpgasvrvsckasgytfidsy-ihwirqapghglewvgwinpnsggt 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Gaps
                                                                                                                                                                                                                                                                        MEDLINE; 83065234.
MEDLINE; 83065234.
MINISHTEN H. MINISHTON M., DEPRYSHIPE P.B., VINEY J. BELL L.O., GOTHER H. J. PROC. NATL. ACAD. SCI. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                              RENNICH H.H., JOHANSSON S.G.O., VON RAHR-LINDSTEOM H.;
INI IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELLOPMENTS,
BACH M.K., ED., PP.L.-1-8, MARCEL DEKKER, NEW YORK, (1978).
--- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VEPTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION (ND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 458; DB 5; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.28e-74;
24; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                               21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECIPSOR V-I PEGION (ND) (FPAGMENTS).
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN PEF 2).
MISSING (IN PEF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6D605E13 CRC32;
                                                                                                                                           143 AA
                                                                                                                                         PPT;
                                                                                                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN V REGION; SIGNAL.
NON_CONS 1 5
SIGNAL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16051 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 53.8%;
les 70; Conserved
                                                                                                                                           STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                            PIR; A02025; ElHUND.
HSSP; P01607; 1FGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
121
143
143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 gggttvtvss 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 GQGTLVTVSS 127
                                                                                                                                                                                                                                       EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 16-142.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                      119 tllivss 125
                                                                                            121 TLVTVSS 127
                                                                                                                                         HV1C_HUMAN
P01744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
MOD_RES
DISULFID
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CONFLICT
NON_TER
SEQUENCE
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79 ynekfkgkttltvdkssstaymqlrsltscdsavyfcar---sh-y-yggsydfdywggg 133
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SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 evgl-ggsgaelvkagssvkmsckatgytfssyelywvrgapgggledlgyissssaypn 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 evgl-ggsgaelvragssvkmsckasgytftsyginwvkgrpggglewigyinpgngyin 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCIENCE 216:309-311(1982).

EMBL; JOO493; G195007; -.

FIR; AC02028; HVMSG7.

HSSP; P01789; 6FAB.

IMMUNGGLOBULIN V FEGION; ANTIARSONATE ANTIBODY; HYPPIEGMA; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA, CHORDATA, VEPTEBPATA, TETRAPODA, MAMMALIA,
EUKAPYOTA: METAZOA; CHOPDATA; VEPTEBRATA; TETPAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A/J;
MEDLINE; 8:152818.
SIMS J., PABRITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.
CAPRA J.D.; --- 1111000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V PEGION (93G7)
                                                                                                                                                                                                                                                                                                                                                                                                  Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 48.1%; Score 448; DB 5; Length 140; Local Similarity 55.9%; Prod. No. 3.58e-72; es 71; Conservative 20; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Score 456; DB 5; Length 114;
Pred No 6.31e-74;
13; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 yaqkfqgrvtitadestntaymelsslrsedtavyfeavrvi 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY
                                                                                                                                                                                                                                                                                                                           NON_TER 114 114
SEQUENCE 114 AA; 12555 MW; 1A027FID CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 AA; 15514 MW; 0700D5C8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
10-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PPECURSON V PEGION (93G7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 AA.
                                                                                            STRAIN=A/J;
MEDLINE; 79195438.
CAPRA J.D., NISONOFF A.;
J. IMMUNOL. 123:279-284(1979).
                                                                                                                                                                                                                                                                                                                                                                                             Match 19.0%;
Local Similarity 69.6%;
les 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
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HSSP; P01772; 1FGV.
                        EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                    SEQUENCE.
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HV02_MOUSE
P01746;
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SEQUENCE
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                                                                      SECTIENCE
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20 qvql qqpqaelvkpqasvklsckasqytftsywmhwvkqrpgrglewigridpnsggtk 78
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ROTHWELL A L M . PASKIND M . RFTH M . IMANISHI-KARI T . BAJEWSKY K .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION (B1-F / 186-2)
                                                                                                                                                                                                                                                                                                                                                                                           CELL 24:625-637(1991).
-!- THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYRPIDOMA MAKING
-!- THE B1-8 TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
HV07_MGUSE STANDARD; PRI; 139 AA.
P01751; P01752;
21.JUL-1986 (REL. 01, CREATED)
21.JUL-1986 (REL. 34, LAST SEQUENCE UPDATE)
61-GCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
MUS MUSCULOS (MOUSE).
EUKARYOTA, METALOR CHORDATA: VEPTERRATA; TFTRAPODA: MAMMALIA:
EUKARYOTA, METALOR.
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EUKARYOTA: METAZOA; CHORPATA: VERTEBRATA: TETPAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r Match 45 4%; Shore 423; DR 5; Length 139; Local Similarity 51 2%; Frod No. 1 160-66; Local Similarity 51 2%; Mismatches 28; Indels nes 65; Conservative 27; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JAN-1940 (REL 16, LAST SANOIATION UPDATE)
IG HEAVY CHAIN PRECURSOR V REGION (VHSS8 AL/A4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15419 MW: DEB2C7DA CPC32;
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BY SIMILARITY.
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SIGNAL 1 19 19
CHAIN 20 139
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CELL, 40.271-281(1985).
EMBL: M13787; G466291; -..
PIR; A02029; HVMSA1.
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HSSP; P01810; 1JHL.
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139 1
139 AA;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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118
125
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HV52_MOUSE
P06327;
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SEQUENCE
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DISULFID
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DOMAIN
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Query Match 44.1%; Score 411; DB 5; Length 119; Best Local Similarity 50.0%; Pred. No. 4.90e-64; Matches 64, Conservative 31; Mismatches 23; Indels 10, Gaps
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                                                                                                                                                                                                                                                                                                                                                 Sapes
                                                                                                                                                                                                                                                                                                                                                                                              20 gygl-ggsgpelykpgalykisckasgytfusydinwykgrpggglewidwiypgdgstk 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVOLLEGSSAEVKKPSSSVKVSSOVFSSTFSFYTIOMLROAPGOGPEWRGNIIPVYNIPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gyglv-gsgggvvgpgrslrlscaasgftfsrytihwvrgapqkqlewva-vmsyledbyk 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVÖLLEUSGAEVKKPGSSVKVSCOVFGIVTFSPYTTOWI POAPGOGPEWMGNITPVY-NTP-59
                           IS BEAVY CHAIN V PECTON (VESSE ALZA4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA: METAZGA: CHORDATA: VEKTFRKATA: TFTKAPODA; MAMMALLA:
EUTHERTA: PRIMATES.
                                                  FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                                                                          COMPLEMENTARITY DETERMINING 2
                                                                                                                                                                                                                                                                                         Query Match 44.1%; Score 411: DB 5: Length 117: Best Local Similarity 56.6%; Pred. No. 4.90e-64; Matches 56, Conservative 20, Mismatches 22, Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPERENT CONTRACT J. PRICHEL W. HILSCHMANN N.;
HOPPE-SEXLEP'S Z. PHYSIOL, CHEM 357:1515-1540(1976).
-1- THIS CHAIN WAS ISOLATED FROM AN 1GG1 MYELOMA PROTEIN.
PIE: A02053; G1HUNI.
HSSP. POLGOJ. LEGV.
IMMUNGIORUIN V PEGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHEM 357:1571-1604(1976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 ynekfkgkatltadkssstaymqlssltsensavyfear 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12971 MW; A60F2B13 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 AA; 13242 MW; 5703CA8E CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (PEI 01, IAST SEQUENCE UPDATE)
21-JUL-1986 (PEL 01 LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 AA
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                                                                                                                                                                                     BY SIMILARITY.
                                                                                                       FRAMEWORK 2.
                                                                                                                                                      FPAMFWOPK 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PONSTINGL H., HILSCHMANN N.; HOPPE SEYLER'S 2 PHYSIOL C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD:
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1119
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117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
                                                                                                                                                                               41
117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE: 77070269.
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HV1D_HUMAN
P01760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV3I_HUMAN
P01770;
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DISULFID
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DISULFID
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  SIGNAL
                      CHAIN
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78 gyngkfkskatltrdnssstaymelssltsedsanyyear 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA; 12972 MW; 9410002E CRC32;
                                                                                                                                                                                                                                                                                                                               21-701-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-0-01-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMUNOSLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 43.8%;
Local Similarity 56.0%;
es 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HV06_MOUSE STANDARD;
P01750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, J00488, G554028; F. PIR, A02041; HVMS8A. HSSP, P01789; 11G1
                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIP; ACECAE; HVMSC
HSSP; PO1810; LUHL
                                                                                                                                                                              132 tlvtfsa 138
                                                                                                                                                                                                  121 TLVTVSS 127
                                                                                                                                                                                                                                                                          LT 14
HV14_MOUSE
P01758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches 38; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLLEQSGAEVKKPGSSVKVSCQVPGUTPSRYTTUWLPLAPGGGPFWMGNTFPVYNTFN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDILINE: 84248078.
GILLIAM A.C., SHEN A., PICHAPDS J.E., BLATTNEP F.P., MISHINSKI J.F.,
TUCKEP P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gvglm-gsgaevkkpgssvrvscktsggtfvdykglwvrgapgkglewvggiplrfngev 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION (TEPC 1017).
                                                                                                                                                                                                                                   -!- THIS CHAIN WAS ISCLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o i
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23-0CT-1986 (REL. 02, LAST SEQUENCE UFDATE)
01-ANS-1992 (REL. 02, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PPECTYSOP V PEXION (TEPT 1017).
MUS MUSCUUS (MOURE).
EUKARYOTA: METACOA: CHOPDATA: VEPTERPATA. TETPAPOGA. MAXMALIA.
                                                                                                  CHORDATA, VERTERRATA, TETRAPODA, MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING 3.
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Pred No. 1 346-63;
26; Mismatches 09: reast
                                                                                                                                                                                                                                                                                                                                                                                                         Score 411; DB 5; Length 124;
Pred. No. 4.90e-64;
                                                                                                                                                                                                                                                                                                                                      PYFRACIE NE CAPRIXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROC NATL ACAD, SCL. U.S.A. 81-4164-4168(1984)
PIP, ACAD3: HWWET7
HSSP, PO1810: 1JHL.
IMMUNOGLOBFLUN V PEGION; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 FPAMEWOPK 4
115 RY SIMILABITY
138
15576 MW: BEF6247B (PC32);
                                                                                                                                                                                                                                                                                                                                                      124 124
124 AA: 13694 MW: 479BD2BE CRC32:
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE (PETATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPEATE)
15 HEAVY CHAIN V-1 REGION (MCL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 AA
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                                                                                                                                                                        MEDLINE: 82046599.
ANDREWS D W , CAPRA J D ;
BIOCHEMISTRY 20:5822-5830(1981).
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55 1%;
Matches 70: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 42 98;
Local Similarity 50 48;
les 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD,
                                                                                                                                                                                                                                                                                                                 IMMUNOGLOPULIN V REGION.
                                                                             HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                          PIR; A02043; MIHUWL
HSSP: P01607; 1FGV.
                                                                                                  EUKARYOTA: METACOA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 AA;
                                                                                                                  EUTHEPIA, PRIMATES
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NON_TER
SEQUENCE
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DISULFID
NON_TER
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Best Local S
                                                                                                                                                         SEQUENCE.
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To ynobfundatitydkssstaymqlssltpeofauyyoar---sdgy-y--dw-fvywggg 131
                                                                                                                                                                                             61 YAÇKFQGPLSITADDSTSTAYMELSSLPSEDTAVYFCAPVVIPNAIPHIMGYYFDYWGQG 120
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MEDLINE; 81234548.
BOTHWELL A L.M., PASKIND M., PETH M., IMANISHI-KAPI T., PAJEWSKY K.,
                               | EV_LEGSSAEVKKPSSSSVKVS^_vPrDTFSPYTJØN FQAPSGSPEWMANTEVYNTEN 50
20 gygl-ggpgaelvkpgasyglsckasghtftnywihwvkgrpggglewigeinpndgrsn 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 ergliggsgpelykpgasykisckasgytftdynmhwykgskgkslewigyiypiyagt 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVOLLEDSGAEVKKPGSSVKVSGGVPGFFFSPYTTGWFPGAPGGPEWMGNIIPVYNT-P 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 408; DB 5; Length 117;
Fred No 2.22e-63,
21: Mismatches 20; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BALTIMORE D.:
CELL 24.625-637(1981).
-!- THIS GEMEINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
THAT COULD ENDODE V PEGIONS OF NPR ANTIRODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
1G HEAVY CHAIN PPECUPSOF V FEGION (102).
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA, CHOFDATA, VEPIEPPATA; TETPAPODA; MAMMALIA;
EUTHEPIA: FODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAÎN PRECUPSOR V PEGTON (108A).
MUS MUSCULUS (MOUSE).
EUKAPYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALÎA;
EUTHERIA: NEDRUTEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECTENCE FROM N A MEDITINE, 01245215.
SIVAL P., ZAKOT P., EFFRON K., PECHAVI G., FAM D., COHEN J B. NATUPE 29244264430(1981).
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IG HEAVY CHAIN V REGION (102).
PRAMEMORK 1.
COMPLEMENTATIY-DETERMINING 1.
PRAMEMORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEMORK 3.
BY SIMILARITY.
| 1 | 19 | 15 HEAVY CHAIN V REG | 20 | 117 | 15 HEAVY CHAIN V REG | 20 | 49 | FPAMEWORK 1. | 50 | 54 | COMPLEMENTARITY-DETE | 55 | 69 | 85 | COMPLEMENTARITY-DETE | 86 | 117 | FRAMEWORK 3. | 41 | 115 | 89 | SIMILARITY. | 117 | AA; | 12867 | MW; | 4 BDD1982 CRC32;
  SIGNAL
CHAIN
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Ouery Match
43.8%; Score 408; DB 5; Length 117;
Best Local Similarity 58.8%; Pred. No. 2.22e-63;
Matches 57; Conservative 18; Mismatches 21; Indels 1; Gaps

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Search completed. Tue Feb 24 07.04.39 1998 Job time: 24 secs.

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Release 2.1D John F. Collins, Biocomputing Research Ubit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tie Feb 24 07-04:59 1998: MasPar time 8.21 Seconds 471.531 Million cell updates/sec Pun on.

Tabular output not generated.

>US-08-844-215-2 (1-127) from US08844215.pep 931

1 EVÜLLEÇSGABVKKPGSSVK Description: Perfect Score: Sedneuce:

. HIMGYYFDYWGQGTLVTVSS 127

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir53 Database:

lianni 2:anni 3:anni 4:anni 5:unanni 6:unanni 7:unanni 8:unanni 9:unanni 10:unanni 11:unanni 12:unanni 13:unanni 14:unanni 15:unannii 16:unannii 17:unenc

Mean 41.781; Variance 118.597; scale 0.352 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred No.
				-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
٦	658	70.7	CA	7	-	Ig heavy chain V-1 r	1.46e-74
Ci	658	0	Cq	7	PH0955	heavy chain V r	1.45e-74
٣	631	~	129	7	A33548	19 heavy chain V-1 r	1.11e-70
4	625	Γ.	C3	۲-	PH0957	Ig heavy chain V req	8.08e-70
'n	624	~	< ₹	۲~	10	g heavy chain V	1.126-6
9	622	S	C1	۲-	PH0958	Iq heav; chain V req	2.180-
7	613	65.8	128	^	PH0952	q heavy chain V	4.25e-
<b>c</b> c	605	S	$\omega$	7	S46394	ъ	5.95e-6
σ	604	4	3	7	C33548	q heavy chain V-	8.27e-6
10	504		527	7	\$14683	Ig mu chain precurso	8.27e-6
11	603		2	۲	S44108	g heavy cha	1.15e-66
12	299	64.3	3	7	PH0954	6	4.30e-6
13	296	•	122	7	59	g heavy chain V	1.15e-6
14	586		Н	7	4410	ь	3.11e-6
15	578		116	٢	9	Ig heavy chain V req	4.31e-63
16	578	62.1	136	7	96	q heavy chain V	4.31e-6
17	572	61.4	α σ	r	\$26915	heavy chain V	3.10e-6
18	572	61.4	116	_	Ç,	g heavy chain V	(۲)
19	572	61 4		7	g.	g heavy chain pre	3.100-6
20	572	51.4	611	7	96	g heavy chain v r	3.10e-6

120 ttvtvss 126 | | | | | | | | 121 TLVTVSS 127

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PH0953 A32483 S24680 A49590	196 495 116 464	3352 335 1HU H08 H08	B32274 PN0536 S31667 PH1666 A30523	535555 53555 PH1671 PH1667 PH1667 S29257 FL0105
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## ALIGNMENTS

SULT 1  TRY 1933548 #type complete GANISM   formal_name   homo sapiens #common_name man   17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change   16-Aug-1996   formal_name   homo sapiens #common_name man   17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change   16-Aug-1996   formal_name   homo sapiens #common_name man   17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change   16-Aug-1996   formal_name   17-Jan-1990 #text_change   16-Aug-1996   formal_name   17-Jan-1990 #text_change   16-Aug-1996   formal_name   17-Jan-1990 #text_change   183354   formal_name   183354   formal_name   18354   formal_name   18355   formal_name   18355   formal_name   18355   formal_name   18356   formal_name   18357   formal_name	1 gvglv-gsgaevkkpgssvkvsckasggtfssyaiswvrgapggglewmgglipligtan 59 
RESULT 1 EDITE TITLE ORGANISM DATE DATE ACCESSIONS REFERENCE #authors #journal #title #ccession #status #statu	Db 1 qvq1:   :    Qy 1 EVQL

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Proc. Natl Arad Sci U S A (1989) 86:5913-5917
Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
                                                                                                                                                                                                                                                                                                                                               *superfamily immunoglobulin V region: immunoglobulin homology
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                                                                                                                                                                #authors Martin. T : Duffy, S F · Carson. D A · Kipps, T T
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies
#cross-references MUID:92202880
                                       Ig heavy chain V region (G6+ CLL-AND) - human (fragment) #formal_name Homo sapiens #common_name man 17-Apr-1993 #text_change
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#journal J. Exp. Med. (1992) 175:983-991
#iitle Evidence for somatic selection of natural authoriticalises.
#cross-references_MUID:92202880
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Carson, D.A.
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#region framework 2\
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Local Similarity 72.7%;
Nes 93; Conservative
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1-129 ##label MAR #superfamily immunoglobulin homology
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#superfamily immunoglobulin V region; immunoglobulin homolody
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Ig heavy chain V region (64- CLL-BRA) - human (fraument)
#formal_name Homo sapiens #common_name man
17.Apr.1993 #sequence_revision 17.Apr.1993 #formage
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#journal J. Exp. Mcd. (1992) 175:983-991
#tille Evidence for somatic selection of natural autoantihodies.
#cross.references MUID-92202880
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Pred. No. 1.11e-70;
17; Mismatches 17; Indels
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nes 92; Conservative
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1-128 **label MAR *superfamily immunoglobulin homology *superfamily immunoglobulin V region: immunoglobulin homology
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#journal J. Exp. Mrd. (1942) 175-983-991
#title Evidence for sometic selection of natural autoantibodies.
*cross-references MUID-92202880
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Pred No 4.25e-68;
15; Mismatches 20; Indels 3; Gaps
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#formal_name Homo sapiens #common_name man
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#region complementarity-determining 1\
                                                     Query Match 66.8%; Score 522; DB 7; Length 122; Best Loral Similarity 73.2%; Prod No. 2.186 Fo; Matches 93; Conservative 15; Mismatches 14; Indels
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#length 128 #checksum 3537
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'-has 91; Conserve
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#journal J. Exp. Med. (1992) 175.383-991
#fille Evidence Somatic selection of natural autoantibodies
#cross-references WUID:52202880
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J. Exp. Med. (1992) 175:983-991
Evidence for somatic selection of natural autoantibadies
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Ig heavy chain V region (5+ T-L42) - human (fragment)
#formal_name Home septiens #common_name man
17-Apr-1992 #sequence_revision 17-Apr-1993 #text_change
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#region complementarity-determining 3
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Carson, D.A.

Proc. Natl Acad Sci U S A. (1989) 86:5913-5917
Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic
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FICATION #superfamily immunoglobulin V region, immunoglobulin homology
DS heterotetramer; immunoglobulin
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J. Mol. Biol. (1994) 239:68-78
In vitro assembly of repertoires of antibody chains on the
surface of phage by renaturation.
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#formal_name Homo sapiens #common_name man
17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
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#length 133 #molecular-weight 14320 #checksum 1289
                                                                                                                                                                                                                                                                       #domain immunoglobulin homology #label IMM #length 132 #molecular-weight 14293 #checksum 7515
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                                                                                                                                                                                                                                                                                                                                              Length 132;
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Pred. No. 5.95e-67;
18; Mismatches 17; Indels
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#accession C33548
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Local Similarity 67.9%;
les 91; Conservative
                                                                                                                                                                                                                                                                                                                                            Match 65.0%;
Local Similarity 68.4%;
les 91; Conservative
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#residues 1-123 ##label HAW ##cross-references EMBL:Z31397 FICATION #superfamily immunoglobulin V region: immunoglobulin homolody
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FICATION #superfamily immunoglobulin C region; immunoglobulin homology
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Idiotypic vaccination against human Brccll lymphoma :rescue
of variable region gene sequences from biopsy material for
assembly as single chain fv "personal" vaccine.
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           Ig mu chain precursor, membrane-bound (clone 201) - human #formal_name Homo sapiens #common_name man 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVÖLLEQSGAEVKKPGSSVKVSCQVFGDTFSRYTIOWLRQAPGGGPEWMGNIIPVYNTPN 60
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#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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#length 627 #molecular-weight 68510 #checksum 8581
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gth 122 #molecular-weight 19307 #rbooksum
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Pred. No. 8.27e-67;
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#cross-references MUID:90332450
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Best Local Similarity 67.9%;
Matches 91; Conservative
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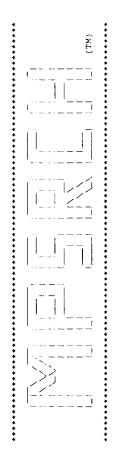
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1-132 ##label MAR #superfamily immunoglobulin homology
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Ig heavy chain V region (ACHSVI, clone 18) - human (fragment)
Heformal_name Homo sapiens #common_name man
06-oct-1994 #sequence_revision 18-Nov-1994 #text_change
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                                                                                                                                                                 PHO954 *type fragment
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
#formal_name Homo sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1995
                                                                                                                                                                                                                                                                                                                                   #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med (1992) 175-983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
1 qvqlv-qsqaevkkpgssvkvsckasqqtfssyalswvrqapqqqlewmggllplfgtan 59
                                    1 EVQLLEQSGAEVKKPGSSVKVSCQVFGDTFSRYTIQWLRQAPGQGPEWMGNIIPVYNTPN 60
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Recombinant human Fab to glycoprotein D neutralizes
infectivity and prevents cell-to-cell transmission
herpes simplex viruses 1 and 2 in vitro.
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#region complementarity-determining 2\
#region framework 3\
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#length 132 #checksum 9232
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Pred. No. 4.30e-66;
16; Mismatches 19.
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#accession B49590
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Best Local Similarity 68.4%;
Matches 91; Conservative
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*superfamily immunoglobulin V region; immunoglobulin homology
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FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                         1 leesgaevkkpgssvkvscrasggtfnnyaiswvrqapggglewmggifpfrntakyagh 60
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19 heavy chain V-J region - human
#formal_name Homo sapiens *common_name man
13-Jan-1995 *sequence_revision 13-Jan-1995 *text_change
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#formal_name Homo sapiens #common_name man 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Aug-1996
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12, Mismatches 21, Indels
                                                                                                                                                                                                                  Score 596; DB 7; Length 122
                                         ##experimental_source bone marrow lymphocytes
##note sequence extracted from NCBI backbone
                                                                                                                                                                                                                                                                17, Mismatches 18;
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                                                                                                          heterotetramer; immunoglobulin
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1-122 ##label BUR
                       ##cross-references NCBIP:141851
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Best Local Similarity 70.9%;
Matches 83; Conservative
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Matches 86; Conservative
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##status preliminary; nucleic acid sequence not shown
##molecule_type mRNA
##residues 1-116 ##label GRI
##residues EMBL:218841

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
                    Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
Embleton, M.J.; McCafferty, J.; Baier, M.: Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
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                                                                                                                  EMBO J. (1993) 12:725-734
Human anti-self antibodies with high specificity from phage
display libraries.
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Best Local Similarity 69.5%; Pred. No. 4.31e-63;
Matches 82; Conservative 14; Mismatches 19; Indels 3; Gaps
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                                                                                                                       #journal
#title
                         #authors
REFERENCE
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US-08-844-215-2.rai



Release 2.1D John F. Jollins, Biocomputing Pessarch Usit Copyright (~) 1947, 1944, 1945, University of Edinburgh, U.K Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tup Feb 24 07 33.22 1998. MasPar time 3.39 Seconds 190.958 Million cell updates/sec Tabular output not generated. Pon on

>US-08-844-215-2 (1-127) from US08844215.pep 931

HIMGYYFDYWGQGTLVTVSS 127 1 EVQLLEQSGABVKKPGSSVK Description: Perfect Score: sedneuce:

PAM 150 Scoring table. 56402 seqs, 5095871 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-issued 1.backi 2.51 3.52 4.53 5.54 6.55 7.56 8.PCT90 9.PCT91 10.PCT92 11.PCT93 12.PCT94 13.PCT95 14.PCT96

Mean 20 207; Variance 150,259, scale 2:180 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result No.	Score	Query	Query Match Length	UB	I.	Description	Pred. No.
	616	66.2	147	ري ا	-212-80-82	Sequence 4, Application	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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### ALIGNMENTS

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COPPESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OFERALING SYSTEM: PC-PUS/MS-DOS SOFTWARE PARCHIE PARCHAGE #1.0. Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                         APPLICANT: LAKE, PHILIP
AFFLICANT CSTRENG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
          147 AA.
                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
FRNCE 147 AA, 10801 MW, 103306 CN;
          PRT;
                                                                                           Sequence 4, Application US/08217918
Fatent Mo. 5506132
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   ATTOPNEY AGENT INFORMATION:
NAME: Smith, Willaim M
ESSISTRATION NUMBER: 30,223
TELEFORMUNICATION INFORMATION:
TELEFHONE: (415) 226,240
INFORMATION FOR SEQ 10 NO. 4.
                                                                        Sequence 4, Application US/08217918.
                                                                                                                                                                                                  379 Lytton Avenue
                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 147 amino acids
TYPE: amino acid
          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      COMPITER FEADABLE FORM MEDIUM TYPE. Floppy
                                                                                                                                                                                                             Palo Alto
: California
RY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                              94301
  T 1
US-08-217-918-4
                                                                                                                                                                                                                                   COUNTRY:
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                                                  01-JAN-1900
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RESULT
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VARIABLE PEGLON GENE FAMILY PESTRICIED ANTIROPIES
                                                                                                                                                                                                                                                                                                                                                                                            VACCINATION WITH A B-CELL SUPERANTICEN AND CONJUG
                         'n,
                                                                                                 79 YAQKFQGRVT1SADASTSTAYMELSSLPSDDTAMYYCAHDITAPGAAPTPLNFYGMDVWG 138
                                                                                                             20 QUÇLV-QSGAEVKKP3SSVKVSFKASGGTFSNPATSWVPDAPGGGLEWMGFIMPLFVTSI 78
                           Gaps
Score 616, DB 6; Length 147,
Pred, No. 5.42e 39;
18; Mismatches 12; Indels 3:
                                                                                                                                                                                                                                                                                                                                                         METHOD FOR STIMULATING PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IRW PC compatible
SYSTEM: PC-POS/MS-DOS
Paten*ID Pelease #1 0, Version #1.25
                                                                                                                                                                                                                      120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      F. Spensley Horn Jubas & Lubit:
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER. PCT/USG //10555
29-0CT-1993
                                                                                                                                                                                                                        PFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMHNICATION INFORMATION
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                     Sequence 12, Application PC/TUS9319555
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                               Sequence 12, Application PC/TMS9310555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
LOCATION: 1 120
NGE 120 AA: 12944 MW: 80844 CN:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Howells, Stacy L. REGISTRATION NUMBER: 34.842
                                                                                                                                                                                                                                                                                                                                                                                                                     THEREOF
                                                                                                                                                                                                                        STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTOPNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
Query Match 65.2%;
Best Local Similarity 65.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
COPPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                         86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: TRM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                139 QGTTVTVSS 147
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P:T1-US$3-10555-12
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60 AGKEGSPVIITTDESTSTAYMEVSSI RSEDTAL/YYCAREGRRMAI-NP----FPYWGGGT 114
                                                                                                                                                                                               62 AGKEGSFLS-11ADGSTSTAYMELSSLFSBLTAVYFCAPVVLPNALBHTMRYYFDVWRGGT 121
                                                                                1 VollV-GSGAFVKKPGSSVKVTGKASGDTFSSSAISWVPQAPGGG1FWMGG11D1FGTPNY 59
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bendig, Mary M.
APPLICANT: Leger, clivier J.
APPLICANT: Saldanha, Tose
APPLICANT: Jones S. Tarran
TITLE OF INVENTION: Homesized Antibudies Anains! Institute OF INVENTION: Adhesion Molecule VLA-4
Tength 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lengar B. 129:
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                                         10001
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                                                                                                                                                                                                                                                                                                                                                    129 AA
                                         14; Mismatches 15.
  Score 602; PB 11;
Pred. No. 6.85e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.6%; Score 583; DB 13;
69.2%; Pred. Nc. 2.13e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHIMMES. CURRENT APPLICATION DATA:
APPLICATION NUMREP. PCT/HSGS/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                       PPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFFLICATION NUMBER: US UB/186,269
FILING DATE: 25-JAN-1994
ATTOPNEY/AGENT INFOPMATION:
NAME: Smith, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45, Application PC/PHS9501219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45, Application PT/THS9501219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEPATING SYSTEM: POSTOG/MS-TOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 129 AA; 13930 MW; 96169 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEFEPENCE/DOCKET NUMBER 15.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
Query Match
Best Local Similarity 72.28;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER FRADARIE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER ÜF SEĞUENCES: 4
ÇOPPESPONDENCE ADDPESS:
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEGISTRATION NUMBER
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Bost Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94105
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                                                                                                                                                                                                                                      115 LVTVSS 120
                                                                                                                                                                                                                                                                        122 LVTVSS 127
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Matches
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TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VAPIABLE PROJECT SENE FAMILY PESTRICIED ANTIGODIES
                                                                                                                                                                                                                                                                       TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPEPANTIGEN AND CONTING
                                                              60 NYAQKEQGPVTTTADTSTSTAYMELSSLESSDFAVYYGABABSYGSGGYYRGHYXFLVW 119
               Length 120;
Matches 90; Conservative 11; Mismatches 25, Indels
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENI APPLICATION DATA:
                                                                                                                                            120 AA
                                                                                                                                                                                                                                                                                                                  E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 62.29; Shore 579, 38-11, Best Local Similarity 67.58; Pred. No. 4.40e-36,
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCI/US93/10555
FILING DATE: 29-OCT-1993
                                                                                                                                            PPT
                                                                                                                                                                                                                  Sequence 13, Application PC/TUS9310555 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IRM PC compatible
OPERATING SYSTEM: PCT-LOS/MS-FOS
                                                                                                                                                                                               Sequence 13, Application PC/TUS9310555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10N: 1, 120
120 AA: 13008 MW: 78865 CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IELEPHONE: (619) 455-5100
INFORMATION FOR SEQ. ID NO. 13.
SEQUENCE CHARACIERISTICS:
LENGTH. 120 amic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
PEGISTPATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEFERENCE/DOCKET NUMBER FD TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                        THEPEOF
                                                                                                                                            STANDAFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide IMMEDIAIE SOURCE: CLONE: RAS FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                         COPPESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
LOCATION: 1.120
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                       120 GOGTLVIVSS 129
                                                                                                         118 GOGTLVIVSS 127
                                                                                                                                  RESULT 4
ID PCT-US92-10555-12
                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                   2 VĢILLEĢISGABVKKPGSSVKVSGQVPGDTFSPYTIQWLPQAPGQCPEWMGNIIPVYNTPNY 61
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Prod No 5 530-35;
14; Mismatches 26; Indels 1, Gaps
  5; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HERPES
TITLE OF INVENTION: SIMPLEX VIRUS AND METHODS THEREFOR
NUMBER OF SEQUENCES: 25
85, Conservative 17, Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible oPPRATING SYSTEM: PC-FASAWS-PAS SOFTWARP: Patentin Pelease #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/00067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: PCT/US95/00067
04-JAN-1995
                                                                                                                                                                                                                                                                                                                                   F.P.T.;
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LOCATION: 1..122
SEQUENCE 122 AA: 12999 MK: 96643 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application PC/TUS9500067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
PEGISTPATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 455-5100
TELEPAX: (619) 455-5110
INPORMATION FOR SEQ 1D NC: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                   STANDAFD;
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Rest Local Similarity 66 7%;
Matches 82, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
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California
RY: USA
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CLONE: FabHSV 8
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PCT-US95-00067-2
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                                                                                                                                                                                                         115 LVTVSS 120
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61 PODRIJITADVSTSTAYMOLSGLIYEDTAMYYCARVAYMLEPTVTAGG-LDVWGQGTTVT 119
                                       5 LEGSGAEVKKPGSSVKVSCOVFGOTESPYİLGMERGAPGGGPEWMSNIIPVYNTPNYAQK 64
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Recombinant Antibodies for Human Therapy NUMBER OF SEQUENCES: 114 CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1 0, Version #1 30
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CITY: Alexandria
                                                                                                                                                   128 AA
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TELECOMMHULCATION INFORMATION:
TELEPHONE: 703-836-6620
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APPLICATION DATA:
FILING DATE. 15-3AN-1395
FILING APPLICATION NUMBER: US 07/912-101
FILING DATE.
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PRIOR APPLICATION DATA:

PRIOR APPLICATION UNIMBER: US 07/735, 054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
TOR APPLICATION:
                                                                                                                                                   PPT:
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                                                                                                                                                                                                                                                  Sequence 63, Application US/08478039 Patent No. 5681722 GENERAL INFORMATION:
                                                                                                                                                                                                                          Sequence 63, Application US/08478039.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Teskin Esq., Pobin L.
PEGISTPATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ 1D NO: 63: SEQUENCE CHARACTERISTICS:
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TOPOLOGY: not relevant
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APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
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PRIOP APPLICATION DATA
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                                                                                                                                                   STANDARD;
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APPLICATION NUMBER:
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                                                                        120 VAS 122
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61 APXFGGRVIXIXDXSXNIAYMELSSLFSEDIAVYYCAFXYGFYSNDYXXXXXYTXDYWAO 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VQLLEQSGAEVKKPGSSVKVSCQVFGDTFSPYTTQWLPQAPGQGPEWMGNTTPVYNTPNY 61
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                                                                                                                                                                                                                                             9; Mismatches 35; Indels 4; Gaps
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
TITLE OF INVENTION: Producing Hotorologous Antibudies
CORRESPONDENCE AFORESS:
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STPEET: One Market Plaza, Stemart Towor, Smito 2000
                                                                                                                                        Score 551; DB 7; Lenath 128;
Fied No. 6.93e-34;
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PEFERENCE/FOCKET NUMBER: 1464 4-9-2
TELECOMONICATION:
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CHECHCSCOME/SEGMENT: VH1 CONSENSUS
SEQUENCE 128 AA; 14138 MW; 114948 CN;
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GENEPAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-UOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 63, Application 20,7059210983.
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JENCE 102 AA; 10940 MW; 55781 CN;
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,;
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AMINO ACID
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AFPLICATION NUMBER: FCI
FILING DATE: 19921217
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                                                                                                                                             59.2%;
63.3%;
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California
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Best Local Similarity 77.88.
77, Conservative
                                                                                                                                                                                      Logal Similarity 63 34; es 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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TD PCT-US92-10983-63
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                                                                                                                                             Query Match
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61 YAÇKEÇGELSITADDSTSTAYMELSSLPSEDTAVYEÇAR 99
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Pred. No. 8.30e-34;
9: Mismatches 12: Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lonberg, Nils
APPLICANT: Kay Pobert M
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORPESPONDENCE ABLIRESS: ADDRESSEE: Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER. IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE. Patentin Pelease #1 0, Version #1 25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     102 AA
                                                      64 YAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 YAQKEQGEVIJIADKSISTAYMELSSLESEFITAVYYGAP 102
                                                                                61 YAQKEQGPLSITADDSTSTAYMELSSI. RSEDTAVYECAR 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-10-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 17-7910,279
FILING DATE: 17-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APP-1993
CLASSIFICATION: 800
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APPLICATION NUMBER: IIS 07/990.860
                                                                                                                                                                                                                     PRT;
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MOLECULE TYPE: protein
JENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 63, Application US/08053131
Patent No. 5661016
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 63, Application US/08053131
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SEQUENCE CHAPACTERISTICS:
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415-326-2422
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                                                                                                                                                                                                                     STANDARD;
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COMPUTER PEADABLE FORM -
MEDIUM IYPE: Floppy (
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Watches 77; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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AC XXXXXX

D. JAN-1900

XX Bequence 53, Applic

CC APPLICANT: Ray

CC CANDUTER: DONE

CC CANDUTER: DONE

CC CANDUTER: PADLO

CC COMPUTER: PADLO

CC CANDUTER: SMITH

APPLICATION

CC CANDUTER: SMITH

CC CANDUTER: SMITH

CC CANDUTER: SMITH

APPLICATION

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CC TELEPRAN: ALIC

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CC TYPE: AMINO

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5 QVQLV-QSSAEVKKPGSSSVKVSCKASGGTFSSYAISWVPQAPPGLSLEWMRRIIPILD1DAIAN 53
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Pred No. 8.30e-34;
9, Mismatches 12; Indels 1, Gaps
                                                                                                                                                                                                            APPLICANT: Lonberg, Nils
APPLICANT: Kay, Pobert M
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMBUTER IBM PC COMBALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FCT/US92/06185
FILING DATE: 19910828
  102 AA
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  PRT;
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Local Similarity 77 %%; Pred No P.
es 77, Conservation
                                                                                                                                                                     Sequence 55, Application PC/IUS9206185
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 102 AA; 10940 KW; 55781 CN;
                                                                                                                          Sequence 55, Application PC/TUS9206185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 55, Application US/07834539A
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TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 17654
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SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTOPNEY/AGENT INFORMATION NAME: Smith, William M. PEGISTPATION NUMBER: 8765
  STANDARD;
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AMINO ACID
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CIIY: San Francisco
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US-07-834-539A-55
PCT-US92-06185-55
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STATE:
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                                           APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLLEQSGAEVKKPGSSVKVSCOVFGDTFSPYTIQWLRQAPGOGPEWMGNIIPVYNTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIAN 63
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
59.1%; Score 550; DB 7; Length 102;
Best Local Similarity 77.8%; Pred. No. 8.30e-34,
Matches 77; Conservative 9; Mismatches 12; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application PC/TUS9311612
GENERAL INFORMATION:
APPLICANT: Co. Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L. Selectin
NUYBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000\,
                                                                                                   SSEE: William M. Smith Oner, Suite 2000 San Francisco San Francisco California
                                                                                                                                                                                            OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUPPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 YAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YAQKFQGRLSITADDSTSTAYMELSSI.RSEDTAVFCAR 99
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19920205
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                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
JENCE 102 AA; 10940 MW; 55781 CN;
          Sequence 55, Application US/07834539A Patent No. 5633425 GENERAL INFORMATION:
                                                                                                                                                                       MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-549-9600
TELEPHONE: 415-549-9603
INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                           30,223
                                                                                                                                                                                                                                    FILING DATE: 19920205
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
PEGISTRATION NUMBER: 30.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDAPD:
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHAPACTERISTICS:
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                                                                                  NUMBER OF SEQUENCES: 7
                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TOPOLOGY: lir
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79 YNEKFKGRVIIISDESINTAYMELSSLRSEDIAVYYCAREEYGNYVR-----YFDVWGQG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 58.9%; Score 548; DB 11; Length 140; Local Similarity 65.4%; Pred. No. 1.19e-33; es 83; Conservative 17; Mismatches 21; Indels '
                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/HS93/11612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AA
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STREET: 101 Richmond Street West
                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    11823-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE 140 AA; 15650 MW; 117746 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08264093
Patent No. 5639863
GENERALIANORMATION:
APPLICANT: Michael D. Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08264093.
                                                                    E. Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                  NAME: Smith, William M. REGISTRATION NUMBER. 30,223
                                                                                                                                                                                                                                                                                                                                PEFERENCE/TOOKET NUMBER. 11
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 amino acids
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INFORMATION FOR SEC ID HO:
SEQUENCE CHARACTERISTICS:
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                                                      COMPUTER READABLE FORM.
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TITLE OF INVENTION:
TITLE OF INVENTION:
California
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                    USA
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                                                                          MEDIUM TYPE.
                                                                                                                                                                                        FILING DATE:
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                                  94105
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                COUNTRY:
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RESULT
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                                                                                                                                                                                                                                                                                                                                   E, Gaps
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TITLE OF INVENTION: Humanized Antibodies Peactive with
TITLE OF INVENTION: L-Selectin
UNMER OF SEQUENCES: 12
COPPESPONDENCE ADDRESS:
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SIREET One Market Plaza, Stouart Tower, Sylte 2000
CITY: San Prancisco
STATE: California
                                                                                                                                                                                                                                                                                                          Length 121;
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 *MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS-DOS 6.00
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OPERATING SYSTEM: PC-DGS/MS-DGS
OPERAPE: PAtentin Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/MS/8/11612
                                                                           FILING DATE:
CLASSIFICATION: 536
PPICATION: 536
PPICATION: 536
PPICATION DATA: No. 5639963 applicable dattokney/Adgent INFORMATION:
NAME: Lake, James P.
REGISTATION NUMBER: 31081
PREFERENCE, PROCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        Score 546; DR 7; L
Pred. No. 1.71e-33;
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                                                                 US/E9/264.093
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                                                                                                                                                                                                                                                                                121 AA; 13281 MW; 86979 CN;
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                                                                                                                                                                                                                                                       not applicable
                                                                                                                                                                             TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO. 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                               LENGTH: 121 amino acids
TYPE: amino acid
STPANDEDNESS: not applic
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                                        SOFTWARE: ASCII Editor
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: US/
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Local Similarity 65.4%;
es 83; Conservative
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94105
MEDIUM IYPE:
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APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
IIITE OF INVENTION: IMPROVED HUMANIZED IMMUNOSIOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                      Score 545; DB 11; Length 121
Pred. No. 2.05e-33;
18; Mismatches 21: Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: UJUN-1995
CLASSIETCATION: 424
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA.
APPLICATION WUMBER: US 07/983,946 FILING DATE: 01-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPT;
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBEP: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
                                                                                                                  11823-22
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATINE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
JENCE 121 AA; 13661 MW; 87993 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 104, Application US/08477728 Patent No. 5585089 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 104, Application US/08477728
                                                                   NAME: Smith, William M.
PEGISTPATION NUMBER: 30,223
PEFERENCION/EXET NUMBER: 1182
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                  INFORMATION FOR SEC ID NO: 8: SEQUENCE CHARACTERISTICS: IENGTH: 121 amino acids TYPE: amino acid
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Best Local Similarity 64.6%;
Matches 82; Conservative
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US-08-477-728-104
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US 07/500,274

APPLICATION NUMBER:

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Query Match
Best Local Similarity 76 5%: Pred No 2 93e-33;
Matches 75; Conservative 11; Mismatches 11; Indels 1; Gaps
                                                                                                                                                                                                                                                                                     1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPN 59
                                                                                                                                                                                                                                                                                                   APPLICANT: CO, Man Sung
APPLICANT: SCHBEIDER, William P.
APPLICANT: CANDOLET, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARF: PatentIn Release #1.0, Version #1.25
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ADDRESSEE: Townsend and Townsend and Crew STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                60 YAQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA 97
                                                                                                                                                                                                                                                                                                                                           11823-002600
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APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
                                                       US 07/290,975
                        us 07/310,252
                                                                                                                                                                                                               MOLECULE TYPE: peptide
JENCE 117 AA; 12472 MW; 77871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 72, Application US/08487200 patent No. 5693762 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 72, Application US/08487200.
                                                                                                        TELECOMMUNICATION: TELECOMMUNICATION INCOMMATION: TELECOMMUNICATION INCOMMATION: TELEPHONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 104: SEQUENCE CHAPACTERISTICS: LENGTH: 117 amino acids
                               APPLICATION NUMBER: 05 0/700 PRIOR APPLICATION DATA: 07/290 PRIOR APPLICATION DATA: APPLICATION NUMBER: 05/07/290 PILOR DATE: 28-DEC-1988 ATTORNEY/AGENT INFORMATION: NAME: Smith, William M REGISTRATION NUMBER: 30/223
  FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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California
                                                                                                                                                                                  amino acid
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TOPOLOGY: 111
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1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSRSA11WVRQAPGQGLEWMGG1VFWFGPPN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.3%; Score 543; DB 7; Length 117; 76.5%; Pred. No. 2.93e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                11823-602610
                                                      PRIOR APPLICATION DATA
PRIOR APPLICATION NUMBER: US U7/590,274
FILING DATE: 28 SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13 FEB-1989
PROR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, WILLiam M
REGISTRATION NUMBER: 30,223
APPLICATION NUMBER: 11S 07/634,278 FILING DATE: 19-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY linear
MOLECULE TYPE: peptide
JENCE 117 AA, 12472 MW: 77871 CN:
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                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
TELEFHONE. (415) 335.2400
TELEFHONE. (415) 335.2400
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                PEFFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 117 amino acids
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Best Local Similarity 76.5%,
Annual 75; Conservative
                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
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mutation rate in crucial regions of the viral genome. We have becaratence is evasion of the host immune response through a high disease. A mechanism proposed as being responsible for virus The hepatitis C virus (HCV) is a frequent cause of chronic liver ЯA 60565T EW GEMBYNK-X19611; GENEYNK-X19615; GENEYNK-X19613 SO Gancer Journals; Priority Fournals S.F English AΊ Tournal: Article; (JOURNAL ARTICLE) DL United States CX Qonthal code: KGV, ISSN: 0082-588X. COURNAL OF VIROLOGY, (1995 Jul) 69 (7) 4407-12. OS F30cF06516 (NGI) (CIAIN) 10083IA 089 (GIAIN) S8718IA NC Fome, Italy. Istituto di Ricerche di Biblogia Molecolare P. Angeletti (IRBM), SD O InodesT Scarselli E; Cerino A; Esposito G; Silini E; Mondelli M U; UA viremic hepatitis C virus-infected patients. burative envelope glysoprofein (gp70) hypervariable region lin Occurrence of antibodies reactive with more than one variant of the  $_{
m LI}$ L6FL8796 DИ L67L83S6 N WEDFIKE

corresponding to the sequence derived from the patient described above and the second one synthesized according to the sequence of the HOV BK strain. A high frequency of positive reactions against both HVRI variants was detected in the samples from the viremic individuals. Finally, antibodies cross-reactive with both variants andividuals. Finally, antibodies cross-reactive with both variants padividuals. The present by competitive ELISA in 6 of 10 viremic patients. The potential negative implications of this observation patients.

nonviremis. Two synthetic peptides were used, the first

the same patient. The presence of anti-HVRI antibodies was investigated in a further 142 HOV patients: 121 viremit and 21

amino acids, corresponding to the HVRI sequence found to be predominant in both the serond and third samples, was used as the antigen for detection of antibodies by enzyme-linked immunosorbent assay (ELISA). We observed reactivity against this HVRI sequence in the first serum sample before the appearance of the viral isolate in the bloodstream; the reactivity increased in the second and third the bloodstream; one reactivity increased in the second and third samples while the occurate viral sequence became predominant.

Moreover, our results show that antibodies from all three samples recognize a region mapping at the carboxyl-terminal part of the HVRI and are cross-reactive with the HVRI sequence previously found in and are cross-reactive with the HVRI sequence previously found in

sequenced the hypervariable region 1 (HVEL) of the virus isolated from three serum samples, sollected during 18 months of follow-up, from an asymptomatic HCV-infected patient. A synthetic peptide of 27

for the host are discussed.

- outside of hypervariable region 1. snara o statapedaje sutapeda bedorana od pacearis sampoquaus ILDIA 06562386 WEDFINE 091633866T ИA MISMER I OF 15 MEDLINE  $\Gamma$ 5
- SD Zibert A recymer S; Rispeter K; Meisel H; Kraas W; Jung 3; Roggendorf M; UА
- Institut fur Virologie, Universitatsklinikum, Essen, Germany. ViRology, (1998 Apr 10) 248 (2) 318-21. OS
- Tournal code: XEA, ISSN: 0042-6822.
- Cournal; Article; (JOURNAL ARTICLE) Setated States CA
- $\Gamma$
- Priority Journals; Cancer Journals ESEudlish
- EW L0866T
- EМ
- ЯΑ
- inmunoprecipitation assay to detect the presence of antiviral expressed separately. These three proteins were used in an represents amino acids 584-410 of HVR1 of isolate HCV-AD73, was delta contained no HVRI. As a control, protein pG.HVRI, which 411-688 of E2, respectively, of isolate HCV-AD78; the protein pE2 in vitro translation. They represent aming acids 174-337 of El and hypothesis, two HCV protenns, pEl and pE2 delta, were generated by the induction of virus neutralizing antibodies. To test this offer than the hypervariable region 1 (HVP1) might be involved in eunejobe broteins El and El suddests that parts of these proteins (NCH) staty C statishing the Natified have a statished a very light of the NCH) S040866I
- ed works pEl and pE2 delts ware bested for their ability to were associated with resplution of infection. Rakhit antisera raised or chronic infection, whereas antibodies against protein pG.H9VEL delta did not differ significantly between patients with resolving B-cell epitopes. The antibody responses against proteins pEl and pE2 suggesting that these forms of the HOV envelope profeins contain estraited to aquore drod in beteeteb ad birot attack and partients, liver disease. A high prevalence of antibodies (up to 95.7%) against patiends who later nearless as acute infection or developed chronic (HCV-AD78). Sees were obtained 4-3 months postinfection from antibodies in sers of patients infected with the same isolate of HCV
- .nortbeint antibodies are probably not associated with the resolution of outside of HVPI can induse virus neutralizing antibodies, these cultures. The results suggested that although a few B-cell epriopes neutralize the binding of HCV to susceptible cells in tissue
- 11001036 MELTINE T100108661 ΊÆ ALEMER 3 OF 15 MEDLINE ZΠ
- viral neutralization. Es and significance of hypervariable region 1-specific antibodies in Characterization of antibody response to hepatitis C virus profein ΙŢ
- Institut fur Virologie, Universitatsklinikum Essen, Federal Republic SD Zibert A; Dudziak P; Schreier E; Roggendorf M
- of Germany.
- Journal code: 8L7. ISSN: 0304-8508. ARCHIVES OF VIROLOGY, 1997; 142 (3) 523-34.
- C.I.
- Journal; Article; (JUURNAL ARTICLE)  $\Gamma \cdot L$
- English A.Ι

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suggested replication of HOV in these eells. The significance of spared to the inoquium after infection of behaves HCV. Occurrence of mutations in the nucleotide sequence of HVFI as nemba asse tribrita notice in vitt notice seem asset expending as year viral glycoprotein E2 of hepatitis C virus (HCV) are postulated to Antibodies directed against hypervariable region 1 (HVP1) within the ЯA t0108661 ÆΜ. T0866T EWPriority Journals; Canser Journals EZ

inologaenedadd D&I O-logae and Ic suniv aniladdaen nac ilig Vease fibroblasts suggested that HVR1-specific antibodies in sera obtained and edt of VOH le seibude draments the traited in seibodidas in single patients. Further characterization of the HVFL specific obtained early (< or = 1 year  $\emptyset$  ,i.) and late (up to >) years  $(\cdot,i,\cdot,q)$ HVR1-specific antibodies could be detected in most of the sera (198) preparation was studied. Using immunoprecipitation and ELISA, single-source outbreak by an HCV contaminated and C- immunoglobulin HVRL-specific antibodies in sera of patients who were infelter in a to notrestiestuen ybute of terro ni bestidatee eew eller desidondit

Isobraf A: Melsel H: Kraks W; Schulz A; Jung 9; Roggendorf rsruth g stittedew jo suctipajut butttut-jjes eite vitt pagatiosas at 1 nother additional hypervariable action y region 87.798776 WEDFINE 87398376 ИA

UA

yidh (84%) in this group of patients and most of the patients

up to month 18 p.i. Prevalence of anti-HVPI after 24 nonths p.i. was showed at least two consmoutive anti-HVPl negative early time points within month 7 to 12 p.i. Seven pathents with chronic HOV infections the first a months p.i. and only 5 of 18 sera (25%) were pushive MITH RESPECTIVE time points of sera were anti-HVFL positive within contrast, only 2 of 15 sera (13:) of chronically infected pattents the sera available after 24 months p.i. had such antibodies. In this group of pathents was within month 6 to 12 p.i. (641). Hone if p.t. were anti-HVR1 postitve. The highest prevalence of anti-HVR1 in sqiuom 3 isii; eqi utqim əlqqijana bues qim simijand eniqoedsəi points p.i. In acute self-limiting infections 9 of 81 sera (431) of  ${\sf HCV-specific}$  antibodies were found to be similar at early time wends to smooth bas esmeaseggs dypolatis (820.  $\pm$  9) squonp

their and the second distribution of the second of the second of the contract 17 of 23 partents (74) with chronic disease. The time of appearance if of S8 potimitating scale states and in sections and in the subject of S8 potimitations and in the subject of the subject o were found at least at one time point during the infection course in chronic infection ( $n=\pm 2$ ) were studied. Antibodies directed to HVRL is (8% = 0) printhmit-les soute acute fraction of  $10^{-1}$  m. (6.1.4) HCV-AD78. 307 sera obtained at different time points post infection

peptide to detect antibodies against the main HVPI variant of priedings a paraw bedatidatee asw (ASLIE) Yasaa inedrosonummi besinti-emyzne nA .(87CA-VOH) niinogloonmmi d-ijaa bejanimatnoo VMH a ic etalcal emas edy to betceint need evan chw sineitag

tected to HVPl during the course of infection in a large group HCV isolate in vitro. We analyzed the appearance of antibodies

virus (WCV) have recently been shown to neutralize the corresponding O statusedat it (180H) i mpiper effakiaknaeggá ou bedteethe setboditana

> OS SD

Jeurnal code: GBD: ISSN: 0270-9139. Institut fur Virologie, Universitätsklinikum Essen, Germany. HEPATOLOGY, (1997 May) 25 (5) 1245-9.

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dournal; Article; (JONRMAL ARTICLE)

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AMSWEP 4 OF 18 MEDLINE  $\Gamma \Gamma$ 

Eudlish Journal: Article: (Journal ARTICLE) United States Tournal code: KCV. ISSN: 0022-538X. JOURNAL OF VIROLOGY, (1997 May) 71 (5) 4123-7. Institut fur Virologie, Universitatsklinikum Essen, Germany. Zipert A; Kraas W; Meisel H; Jung G; Roggendorf M I in acute self-limiting and chromic infections due to hepatitus C Epitope mapping of antibodies directed against hypervariable region 99181746 99585076 WEDFIKE MIRMER 2 OF 15 MEDIUME vaccine development. earning for lost producers of the disease and also for any furnite and way and may a self-limiting interaction and may have findings suggest clearance of virus by respective neutralizating maintained high levels of anti-HVP1 for up to 17 years p.i. Cur

It has been postulated that antibodies specific to the hypervariable region I (HVRI) within the putative envelop probein E2 of hepatitis of virus (HCV) can neutralize virus. We studied such antibodies in sera of patients who were infected in a single-source outhreak by a contaminated anti-D immunoglobulin preparation (HCV-AD78). The nucleofide sequences of DDMs encoding HVRI of HCV-AD78 were determined. The four matter a Bacherichta coll. Sixty-seven expressed as fusion professed to HVRI.A, B, C, and D) were expected as fusion professed to HVRI.A. Sera unrelated to expected a losser infection of the outbreak also recognized HVRI.A but to a lesser infection of the outbreak also recognized HVRI.A but to a lesser extent (15°), suggesting that not all HVRI-specific antibodies are absolutely isolate-specific. Antibodies directed against individual variants of HVRI were found in sera obtained searly postinfection (p.i.) (< or = 1 year) but also in sera obtained several years (p.i.) (< or = 1 year) but also in sera obtained several years (p.i.) (< or = 1 year) but also in sera obtained several years

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United States

Priority Journals; Cancer Journals

Tournal; Article; (TOURE:AL ARTICLE)

Virology, (1995 Apr 20) 208 (2) 653-61. Journal code: XEA. ISSN: 0042-6822.

M laobaegges E; Poggendorf M

WEDTIME

Priority Journals: Cancer Journals

AMER 6 OF 15 MEDLINE

Institute of Virology, University of Essen, Germany.

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encyme-linked immunosorbent assay using follow-up sera of patients, all of whom were infected with the same isolate of nepatitis C virus (HCV), our results suggest that (i) an early appearance (up to month is associated with acute self-limiting infections of HCV and (ii) is associated with acute self-limiting infections of HCV and (ii) isolate-independent antibodies which are mainly directed patients forming of HVPl seem to persist in chronically infected patients. The relevance of HVPl-specific antibodies for neutralization was

Epitopes of hypervariable region 1 (HVPL) were mapped by

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evaluated by characterication of a rabbit serum.

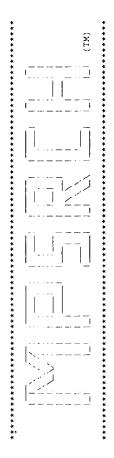
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employed to further characterize these sera. Five of seven sera that were obtained early p.i. prevented binding of HCV to cells. Preincubation of such sera with HVR1-specific fusion proteins restored binding of HCV to cells in four of five sera. These findings suggest that the majority of neutralizing antibodies are directed against HVR1.

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US-08-844-215-16.rng

Page 1



Pelease 2 12 John F. Collins, Biocomputing Pesearch Unit Copyright (c) 1993, 1994, 1995. University of Edinburgh, U.K. Distribution rights by IntolliGenetics, Inc.

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(1-312) from USC@244215.seq 312 >US-08-844-215-16 Description. Perfect Score:

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GGACCAAGGTGGAGATCAAA 312 GCTGGTTGCACCTGTAGTTT

TABLE default Gap 6 Scoring table.

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Listing first 45 summaries Minimum Match 08 Post-processing:

n-geneseq30 Database:

1.part1 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7 8.part8 9.part9 10.part10 11.part11 12.part12 13.part13 14.part11 12.part12 13.part13 14.part17 18.part18 19.part19 27.part28 27.part27 28.part28 29.part28 28.part28 27.part27 28.part28 29.part29 30.part30 31.part31 32.part32 33.part38

Mean 8.010; Variance 4.828; scale 1.659 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

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	Description	DNA fragment vk65.3,	Human V-kappa gene vk	Human DNA fragment vk	Human V kappa gene vk	Human DNA fragment vk	DNA fragmont Vk55.5,	igG light chain varia	1B1 IgG aberrant ligh	Anti-pseudomonas aeru	Anti-P. aeruginosa st	picmb3 expression vec	Expression vector, p?	Anti-tetanus toxoid l	pC3AF313 anti-tetanus	Sequence coding human
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# ALIGNMENTS

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Example 21. Fig 41, 34pp, English.
The present sequence is the variable kappa chain gene segment the present sequence is the variable kappa chain gene segment vectaining human DNA fragment, vk65.3, which was co-injected along with the human DNA fragments vk65.5, vk67.8 and vk65.15 into half day mouse embryo pronoclei, to generate an unrearranged light chain minilocus transgene. The resulting transgenic mice can be used for the production of heterologous (1.e. human) antibodies against specific antigens, this comprises immunising a mouse with a human gamma immunigabulins.
                                            14-APR-1997 (first entry)

DNA fragment vk65.3, containing variable kappa chain gene.

Variable: kappa chain; gene segment; human; DNA fragment; vk65.3;

unrearranged, light chain; minilocus; transgene, transgenic; mouse;

Production, heterologous; antibody; gamma, immunoglobulin, ss.

Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodn. of heterologous human immunoglobulin(s) - by immunising
                                                                                                                                               Location/Qualifiers
.T. 1
T37180 standard; DNA; 812 BP.
T37180;
                                                                                                                                                                                                                                                                                          31-AUG-1990; US-575962
17-DEC-1991; US-810279;
18-MAR-1992; US-853408;
23-JUN-1992; US-990068;
16-DEC-1992; US-990060;
(GENP-) GENNHARM INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                            Kay RM, Lonberd
WPI, 96-383736/
P-PSDB: W03946.
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29-AUG-1990;
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                                                                                                                                                                                    562 aggetecteatetatgatgeatecaacagggecactggeateceagecaggtteagtgge 621
                                                                                                                                                                                                                                        622 agtgggtetgggacagaetteaeteteaceateageageetagageetgaagattttgea 681
                                                                                                      7 ACTEMAGECTECASSEACCETSTOTTSTCTCCASASAAAAAAGACCACCTCTGTGCAGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure: Fig. 41, 296pp. English. Human DNA fragments vk65.3, vk65.8 and vk65.15 (given in Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in LARS2-078955, respectively) wach contain a V-kappa ache sequent that can be used to form a complete human light chain minilous transgene for expression in a nonhuman transgenic animal for sequences of the V-kappa coding regions are given in R6728-R62921. Sequence 812 BP.
                                                   6: Indels 0: Gaps
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                         Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995 (first entry)
Human V-kappa gene vk65.3.
Transgenic mouse, transgenic animal; antibudy engineering; variable region; light chain; minilocus transgene, chimeric antibody; ss.
199 T:
187 G;
                         Score 258; DB 27; 1
Pred. No. 9.25e-158;
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225 C;
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US-209741
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les 264; Conser
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               5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic non-human animals contg. immunoglobulin heavy chain trans gene - used to produce useful antibodics by isotype
                                                                                                                                                                                                                                                                                                                                                                                                 10.NOV-1993 (first entry)

Human DNA fragment vk65.3 containing V-kappa gene segment.

Humanoglobulin: light chain variabie fegich, minilocus;

isotype switching; unrearranged functional Vk gene segment:
human light chain transgene; ss.
               6. Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note "splicing and recombination signal sequences"
Pred. No. 9.25e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          initiation codon, i.e. the start of the ORF; the precise start point of the exon is not indicated.
               Mismatches
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nisc recomb
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/note= "nucleotides 199-201 represent the
                                                                                                                                                                                                                                                                               682 gtttattactgtcagcagcgtagcaactgg 711
                                                                                                                                                                                                                                                                                                          247 GITTATTACTGTCAGTAGGGTAGGGATTGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
199..247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 21; Fig 41; 196pp; English.
                  .;
                                                                                                                                                                                                                                                                                                                                                                       Q44222 standard: PNA; R12 BP.
 Best Local Similarity 97.8%;
Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENP-) GENPHARM INT INC.
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18-MAR-1992; US-853408.
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127 AGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGGATCCCAGGCGAGGTTCAGTGGC 186
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Human DNA fragments vk65 3 vk65 5, vk65 8 and vk65 15 (diven in
Human DNA fragments vk65 3 vk65 5, vk65 8 and vk65 15 (diven in
Human DNA fragments vk65 3 vk65 5, vk65 8 and vk65 15 (diven in
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sequences of the Vkapps and diventage and gives and gives
Sequence 400 RP. Vkapps and diventage and gives 127 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic non-human animals producing heterologous or chimeric antibodies - for binding a pre-determined human antigen with
designated p65.3, p65.5, p65.8 and p65.15 (son 244222-244225,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic mouse; transgenic animal; antibody engineering; variable region; light chain; minilocus transgene; chimeric antibody; ss.
                                    (£) (5) (5)
                                                                  Match 82.7%; Score 258, DB 7, Longth 812, Local Similarity 97.8%; Fred. No. 9.256-178, es. 264; Conservative 0; Mismatches 6; Indels
                                    197 G:
                                    378 63
                                                                                                                                                                                                                                                                                                                                                                                                                         582 gittattacigtcagcagcgtagcaacigg 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 GITTATTACTGICAGCARAGCGRACTGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                    201 A;
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Q78953 standard; DNA; 900 вР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- Recombination_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995 (first entry)
Human V-kappa gene vk65.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-1994; UG-580.
26-APR-1993; US-053131.
22-JUL-1993; US-096762.
18-NOV-1993; US-155301
03-PFC-1993; US-16739
10-DEC-1993; US-165699
09-MAR-1994; US-165699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          696..702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Splicing_signal
misc_signal 715..723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENP-) GENPHARM INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227..395
                                    812 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                increased affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94-359263,144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; P62929
                  respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_signal
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                                    Sequence
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                                                                       Query Match
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                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 aggeteeteatetatgatgeateeaadagggeeactggeateedagoraggiteadiggr 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 agtgggcctgggacagacttcactctcaccatcagcagcctagagcctgaagattttgca 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 AGTGGGICTGGGACAGACTTCACTCTCACCAICAGCAACCTAGAGCCTGAAGATTTTGCA 246
                                                                                                 Sdeb
                                                                                                                                                                                                                                                                                7 ACTOAGIOTOCAGOOAQOOTGTOIIIGAGGGGGAAAAAAAGGGGGGGTGTGGGGGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 21, Fig 42, 196pp, English.

The V-kappa specific cluyeous extribe 760.67 was used to probe a human placental genomic for library cloued into lambdaEMEL/SP6/T7.

ENA fragments containing V-kappa segments from positive plage clones were subclosed into plasmid vectors. Variable gene segments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic non-human animals contq. immunoglobulin heavy chain trans gene — used to produce useful antibodies by isotype
                                                                                                 Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA fragment vk65.5 containing V-kappa gene segment. Human DNA fragment vk65.5 containing V-kappa gene segment. Immunoglobulin, light chain variable region, minliocus, isotype switching; unrearranged functional Vk gene segment: human light chain transgene; ss.
Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "splicing and recombination signal sequence" exon
Score 252, 78 12; 1
Pred. No. 1.46e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiation codon, i.e. the start of the ORF; the precise start point of the exon is not indicated.
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "splicing and recombination signal ?"
misc recomb 696..723
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/note= "ARP not terminated by a stop codon"
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/note= "nucleotides 180-182 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 GITIATIACIGICAGCAGCGIAGCGACIGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 gtttattactgtcagcagcgtagcaactgg 690
                                                                                                                                                                                                                                    Location/Qualifiers
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Query Match
Rest Loral Similarity of 78;
                                                                                                 261; Conservative
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(GENP-) GENPHARM INT INC.
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481 gccagtcagggtgttagcagctacttagcctggtaccagcagaaacctggccaggctccc 540
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                                                                                                                                                                                                                                                                                                                                                        601 agtgggcctgggacagaettcactctcaccatcagcagcctagagcctgaagattttgca 660
                                                                                                                                                                                                                                                                                                                                                                                                                          187 AGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAACCTAGAGCCTGAAGATTTTGCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the variable kappa chain gene segment containing human DNA fragment, vk65.5, which was co-injected along with the human DNA fragments vk65.3, vk65.8 and vk65.15 into half day mouse embryo pronuclei, to generate an unrearranged light chain minilocus transgene. The resulting transgenic mice can be used for the production of heterologous (i.e. human) antibodies against specific antigens, this comprises immunising a mouse with a preselected antigen and collecting antigen binding heterologous Sequence 900 BF; 225 A; 244 C; 204 G; 227 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-ApR-1997 (first entry)

DNA fragment vk65.5, containing variable kappa chain gene.

DNA fragment, vk65.5;

Variable, kappa chain, gene segment; human; DNA fragment; vk65.5;

unrearranged; light chain; minilocus; transgene; transgenic; mouse;

production; heterologous; antibody; gamma; immunoglobulin; ss.
from the resulting cloues were sequenced and functional clones were selected on the basis of open reading frames, intact donor and acceptor splice sites and intact recombination sequences. The sequences obtained from four different plasmid clones were designated p55.3, p65.5, p65.8 and p65.15 (see Q44222-Q44225, respectively).
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of heterologous human immunoglobulin(s) - by immunising
                                                                                                                                       Length 900:
                                                                                                                                                                       9. Indels
                                                                                                          204 6:
                                                                                                                                            Score 252; DP 7; L. Pred. No. 1.46e-153;
                                                                                                                                        DB 7;
                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtttattactgtcagcagcgtagcaactgg 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 GITTATTACTGTCAGCATAGCGACTGG 275
                                                                                                          244 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 21; Fig 42; 94pp; English
                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I37181 standard; DNA; 900 BP
                                                                                                              225 A.
                                                                                                                                          Ouery Match
Best Local Similarity 96.7%;
Matches 261; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-12-...
31-AUG-11990; US-575902.
17-DEC-1991; US-810279.
18-MAR-1992; US-853408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENP-) GENPHARM INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398..693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-574748.
US-575962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1992; US-990860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96-383736/38.
                                                                                                              900 BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB, W03947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5545806-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ω
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                                                                                                                 Seguence
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421 acacagictecagecaeceigletligletecayyyyauagageceteierignayg 480
                                                                                                                                                                                                                                       601 agigggeetgggaeagaetteaeteteaceateageageetagageetgaagatiligga 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                       Claim 43; Fig 17: 104pp; English.

The leader peptide and the L'V region are encoded in different reading frames. The L'V region corresponds to the last three amino acids of the leader peptide and the rearranged VJ gene. Clone 4B9-Vk15 (see Q11878) encodes an aberrant light chain containing two such L'V regions.

See also Q11880.
                                                                       Indels 0; daps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligomeric immunoglobulin(s) with high avidity for antiden(s) tormed by duplicating esp. variable region of light chain of Igg
                                                                                                                                                 igs light chain variable region clone.
Immunogiobulin G, light chain; variable region; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 7:
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                       Length 900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.2%; Score 244, DB 2: Lc
Best Local Similarity 95.2%; Prod No. 5.7le-148;
Matches 257; Conservative 0; Mismatches 13:
Guery Match 80.8%, Stafe 252: PN 27; 1
Best Local Similarity 96.7%; Pred. No. 1.46e-153;
Matches 261; Conservative A. Mirrille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= L'V region
/note= "translates from different reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     passivé immunity, group B streptococci; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 gtttattactgtcagcagcgtagcaactgg 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 GITTALTACTGTCAGGAGGTAGGAGTGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harris LJ, Raff HV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 91-163947/22.
P-PSDB, R12129, P12130, P12131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q11879 standard; DNA; 1204 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRIM ) BRISTOL-MYERS SQUIB. Shuford WW, Harris LJ, Raff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (first entry)
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06-NOV-1990, UC6425.
07-NOV-1989; US-4327
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71 acacagtotocagocacoctgtotttgtotocaggggaaagagcacocototoctgcagg 130
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                                                    67 GCCASICAGAGIGIIAACAAGIACIIAGCCIGGIACCAACAGAAGCIGGCGAGGCTGCC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes an abstrant light chain containing two L'V regions Antibody molecules of the invention can include one or two such abstrant light chains to produce heavier antibodies. These with just a single copy of the L'V region. The clone is not complete; it starts with the G of the AIG initiator codon See also 01879 and 01887. 383 C; 302 G; 266 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligomeric immunoglobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of \rm IgG
                                                                                                                                                                                                                                  1B1 IgG aberrant light chain clone 4B9/Vk15.
immunoglobulin G; light chain variable region; duplication;
passive immunity; group B streptococci: ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 78.2%; Score 244: DB 2; Length 1242; Local Similarity 91.2%; Fred, No. 1.7e-149; hes 257; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                         /label* L'V l
/note= "encodes last 3 amino acids of leader and
                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
/label= L'V 2
/note= "encodes last 3 amino acids of leader and
                                                                                                            931 gtttattactgtcaacaccgtgacaattgg 960
                                                                                                                                     247 STITATIACIGICAGCAIAGGGACTGG 276
                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Shuford WW, Harris LJ. Raff HV
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Q11878 standard; cDNA: 1242 BP.
Q11878;
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/*tag= d
/note= "constant region"
interior interior
                                                                                                                                                                                                                       (first entry)
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06-NOV-1990; U06426.
                                                                                                                                                                                                                                                                                                                                                                                                      the rearranged VJ
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                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "leader"
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P-PSDB; R12128
                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                         siq_peptide
                                                                                                                                                                                                                     01-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                     misc RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_RNA
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                                                                                                                                                                                                                                                                                                                                                misc RNA
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contains constant kappa and lämbda type regions, and versatile region recognising psacruginosa R4 and H1 types begon the pages 510-511 129ps Japanese. It also codes for a variable region recognising Ps.aeruginosa F4 and H1 types. The Ab can be used for immunologic control of infection caused by Ps.aeruginosa. The antibody is made effective against various classes or subclasses of resistant Ps aeruginosa by recombining corresp DNA L-chain
644 gccagtcagagtgttagcagcaattecttageetggtaenaanagaaanetggnnaggn 703
                                                        251 agigggiritgggaragacticarititarratosgcagoctagagootgaagattitgoa 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 ACTICAGICICCAGCCAGCCIGICILISICICCAGGGGAAAGAGGCACCCIGTGCTGCAGG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.48, Spore 232, DB 2, Length 1911,
90 08: Pred No. 1369-139,
Jailve A, Mismatches 28, Induls 3, Saps
                                                                                                                                                                                                                                      Anti-pseudomonas aeruginosa human type antibody L-chain coding DNA contg constant region of kappa and lambda types
Pseudomonas aeruginosa F4: Pseudomonas aeruginosa H1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 88-216877/31.
P-PSDB; P81246, P81245.
Anti-Fseudomonas aeruginosa type antibody Lochain coding DNA - Anti-Fseudomonas aeruginosa type antibody Lochain and versatile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 T;
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                                                                                                                 311 gtttattactgtcaacaccgtgacaattgg 340
                                                                                                                                          247 GTTTATTAGTGTGTGAGGGTAGGGAAGTGG 275
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                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Sequence 1011 BP, 237 A,
                                                                                                                                                                                    T 9
N91637 standard; DNA; 1011 BP
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(WAKU-) Wakunaga Seiyaku KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match.

Pest Local Similarity 90 0%.
Matches 278; Conservative
                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                   immunotherapy; ss.
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/note="Claimed SQ"
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/note="P81247"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="P81245"
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/note="L"
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824 gcagtgtattactgtcagcagtacgacgccctgatcactttcggcggagggaccaagttg 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 GSCAGISGSICTGGGAGAGATICACTCTCACCATCACCAACCTAGAGCCTGAAGATTT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production of human IgG monoclonal antibody - by converting human antibody into other subclasses by genetic engineering antibody into other subclasses by genetic engineering pisclosure; fig. 3: 17pp; Japanese.

Disclosure: fig. 3: 17pp; Japanese.

This encodes a variable chain and can be connected to a gene encoding a constant region which determines optional IgG subclass. This can be used to study subclasses, and as an antigen for prepg. IgGl or IgG3 antibod; Regions 32s-372 connected to 560-571 encode the L chain, region 572-856 encodes V chain and region 857-895 encodes J chain. Sequence 1011 BP; 237 A; 263 C; 254 G; 257 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 acgcagictocaggcaccetgictitgictccagggggaagagccaccetetetgcagg 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        644 gccagtcagagtgttagcagcaattccttagcctggtaccaacagaaacctggccaggct 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cccaggetecteatetatgetgegtecageagggeeactggeatercagaeaggtteagt 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 232; DB 1; Length 1011;
Pred. No. 1.36e-139;
0; Mismatches 28; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ACTCAGICICCAGCCACCCIGICITIGICICCAGAGAAAGAGCCACCCICTCCCCCAGG 66
                                                                                                                                                                          824 gcagigiattacigicagcagiacgacgccigaicactiicggcggagggaccaagiig 883
                                  704 eccaggetecteatetatgetgegtecageagggeeactggeateceagaeaggtteagt 763
                                                     ggcagtgggtctggggcagacttcactctcaccatcagtagactggaacctgaagattct 823
                                                                                                                                      184 GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAACCTAGAGCTGAAGATTTT 243
                                                                                                                                                                                               67 GCCAGTCAGAGTGTTA--A-CAAGTACTTAGCCTGGTACCAAGAGAAAGGTGGGGAGGCT 123
                                                                                                                                                                                                                                                                                                                                                                               02-MAR-1990 (first entry)
Anti-P. aeruginosa strain F4 light chain V and J coding regions
Immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
325..372
                                                                                                                                                                                                                                                                                                                                                            N91359 standard; DNA; 1011 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 74.4%;
Local Similarity 90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WAKU) Wakumaga Seiyaku KK.
WPI; 89-303485/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa F4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    560..895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1988; 035395.
19-FEB-1988; JP-035395.
                                                                                                                                                                                                                                                        884 gacatcaaa 892
                                                                                                                                                                                                                                                                                          304 GAGATCAAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
J01211498-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
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Example 1; Page 180-186; 49ypp; English.

Cr his sequence represents the pcomb3 phagemid expression vector. This cyclor has been designed to allow for anchoring of expressed proteins on the bacteriophage coat protein. Fill (cp3), which is expressed the 406 residue minor phage coat protein, cp111 (cp3), which is expressed the 406 residue minor phage coat protein, cp111 (cp3), which is expressed coat protein, cp111 (cp3), which is expressed the 406 residue minor phage coat protein, cp111 (cp3), which is expressed and accumulates on the inner membrane lacing into the peripisan of E. and accumulates on the inner membrane lacing into the peripisan of E. and accumulates on the inner membrane lacing into the peripisan of express coil. This plasmid was used within the scope of the Invention of combinatorial Fab libraries. Prownboard for the relating forms of the Fabs. The vector was designed for the cloning and soluble forms of the Fabs. The vector was designed for the cloning two cassettes to express one fusion protein, Ed/cp3, and one soluble forms of the fabs. The finished vector comprises, operatively protein, the light chain. The finished vector comprises, operatively correction still first cassette consisting of lac2 promoter/operator regions a spacer region, a cloning region bordered by 5 xhol and sequences. A spacer region, a cloning region bordered by 5 xhol and second lac2 promoter/operator sequence. Sequence the two cassettes, and a second lac2 promoter/operator sequence. Collowed by an expression control RBS, a PalB leader, a spacer region. Still and 3 xbal restriction site. The pcomb3 expression vector lorms the basic constitution sites, the pcomb3 expression vector lorms the basic constitution sites. Collowed by a stop codon, a page of 10 minor sequences and a second lac2 promoter/operator regions between the two cassettes, and a second lac2 promoter/operator regions. Collowed by a stop codon and a second lac2 promoter/operator region between the two cassettes, and a second lac2 promoter/operator regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the MT4 Fab display phagemid expression vector, pMT4-3 (see also 092540), used in the invention for the production of synthetic human Fub antibodies against 9pl20 of HIV.
Sequence 4691 BP; 1170 A; 1171 C, 1232 G; 1118 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2677 gageteaegeagteteeaggeacectgtetttgtefreaggqqaaaqqeeueeretefee 2736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2737 igcagggccagicacagigitagcagggcciactiagcciggiaccagcagaaacciggc 2796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TGCAGGGCCAGTCAGAGTGTTAACAAG---TACTTAGCCTGGTACCAACAGAAACCTGGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : GABETTANCTERACTOROGERACOPTESTESTESTESTESTES ANGRARAGE CONTINUE EU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.38e-138;
0, Mismatches 32; indels 4; daps
                                                                                                                                                                                                                                            pcomb3; phagemid expression vector; bacteriophage; coal protein 3; pcomb3; phagemid expression vector; bacterial; cplil; cp3; dene III; filamentous phage; minor phage coat protein; cplil; cp3; bacterial membrane; periplasm; E. coll; human; Fal, HIV, apl20; combinatorial Fab library; cassette; Fdkcp3; lack promoter/kaptrator; ribosome binding site; RBS; PelB leader; spacer; Lether sequence; MT4; pMT4-3; antibody; ss; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunodeficiency virus - used for diagnosis and immuno:thetapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 230; DB 16; Length 4691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic human neutralising monoclonal antibodies to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 185-188; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lerner RA;
                                                                                                                                                       Q92546 standard; DNA; 4691 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                               11-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-0CT-1993; US-139409.
26-APR-1994; US-233619.
19-SEP-1994; US-308841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burton DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCRI ) SCRIPPS RES
Barbas CF, Burton D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-1995.
19-0CT-1994; U11907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-induced disease
884 gacatcaaa 892
                                              304 GAGATCAAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95-170235/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09511317-A1.
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This sequence represents the expression vector, poho-TT which is a modified version of the phagemid expression vector, pcomb3 given in 20256. pphorTT provides for the expression vector, pcomb3 given in 20256. pphorTT provides for the expression vector, pcomb1 are secreted into the periplasmic space which is regulated from the alkaline phosphatase (phoA) promoter This plasmid was used within the scope of the invention to express various mutagenised human Fab's which comprise the unvention to express various mutagenised human Fab's which comprise the avey and light variable regions which bind to HIV gpl20. pcho-TI consists of a DNA molecule having two cassettes to express two soluble promoter/operator sequence, an affect chain. The vector comprises promoter/operator sequence, an affect chain. The vector comprises promoter/operator sequence, an affect cassette consisting of the phoA promoter/operator sequence, an affect restriction site, a rubesome binding site (RBS), an CmpA leader, a Sfil restriction site, a number of sites, an Nool restriction site between the two cassettes, and a second cassette consisting of an expression central stop sequences and a Notle sequence such a not set of sites, and a second consense and mother chain stuffer that is 1200 by in length and a heavy chain stuffer that is 1200 by in length and a heavy and light chains tube heavy and light chains tube heavy and light chains to the heavy and light chains to the consistion of a channer to the control of a person contains of a channer to the control of an expression control sequences and a not a channer to the control of a person control of a person contains a light.
                                                                           2917 gattfigoagistacianigisagsagialgajagsisaongiggisysgosagggass 2974 | HILLIIII | HILLII | HILLII | HILLII | HILLII | HILLIII | HILLII | HILLII | HILLII | HILLII | HILLII | HILLII | HILLIII | HILLII |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4507 gageteaegeagtetecaggeaecetgtetttgtetecaggggaaagageeaecetetee 4666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4667 tgcagggcrantcacagtgttagcagggcctacttagcctggtaccagcagaaacctggc 4726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I.MAR-1996 (first entry)
Expression vector, pPho-TT.
Human. Fab. variable chain, heavy, light; region; VH, VL, HIV, gp120; 3b1; 3b3; 3b4; 3b9; MT4; humanised: monoclonal antibody; MAb; Immunoreaction: neutralisation: passive immunotherapy; tetanus toxin: alkaling phosphatase, phoA, SS, cyclic
118 CAGGGTGCGAGGGTGCTGATGTATGATGCATGTAAGAGGGGTAATAAATGCAGGAAGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGCICACTCAGTCTCCAGCCACCTGTTTGTCTCCAGGGGAAAGAGCCACCTCTCC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic human neutralising monoclonal antibodies to human immunodeficiency virus (used for diagnosis and immunotherapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1415 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.7%; Score 230; DB 16; Length 6166; Best Local Similarity 88.9%; Pred. No. 3.38e-138; Matches 280; Conservative 0; Mismatches 32; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1629 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1705 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Fage 193-197; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burton DR, Lerner RA;
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Sequence 6155 BP; 1415 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .T 12
Q92547 standard; DNA; 6166 BF.
                                                                                                                                                                                                                                                                                                                                                                                                                           2977 aaggtggaactcaaa 2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 AAGGTGGAGATTAAA 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCPI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-1994; US-233619.
19-SEP-1994; US-308841.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV-induced disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-1994; Ullan7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95-170235,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09511317-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-00T-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :7-APR-1995
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diversity antibody libraries, for screening antiques of disk antibody libraries, for screening antiques antibody libraries, for screening antiques antibody libraries, for screening antiques against tender sequence represents the light chain coding sequence derived from the surface display phagement of the light chain variable domains sequences for encoding human feath antibodies against teranus toxin. This sequence was pref. used in the method of the invention for the production of antibody libraries containing increased diversity. The sequences queen in 100480-06 are primers which were used for inducing mutagenesis in a complementary determining region (CDR) of an immorglobulin light chain gene. These primers contain a 3' terminus capable of hybridising to a first framework region and a nucleotide sequence between the 5' and 3' termini having the formula [NNR]n, when the CDR regions of immorglobulins heavy or light chains that the libraries with increased antibody diversity by inducing mutagenesis within the CDR regions of immorglobulins heavy or light chains that the library. These primers filementary by the contain of the library. These primers filements within the library. These primers filements within the library. These primers filements which contain CDR3.
                                        1797 ticagigacagigaginigaganaganitoacinicanodhagcaganigaganigaghnigaa 4846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0/04-APR-1995 (first entry)
Anti-teraus toxoid light chain cDNA from vector, pc3AP313.
Polymerase chain reaction: primer; mutagenesis: PCR: amplify.
diversity: antibody: complementatity determining region: CDR; framework; constant; light; heavy; phage; immunoglobulin, library: ss.
                                                                                                                                                                                                                              121 caggiitoiraggiitoitoitototatatagtacatocagcagggccactggcatoccagacagg 180
61 INGASSOCASICAGACIGIIAACAA:---IACIIAGGIISGIAGGAAAAAACIGGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 tgragggcragtcacagtgttagcagggcctacttagcctggtaccagcagaaacctggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gageteaegeagteteeaggeaecetgtetttgteteeoaggggaaagageeaecetetee 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGCTCACTCAGTCTCCAGCCACCTGTCTTTGTCTCCAGGGGAAA3AGCACCTCLCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 33; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligo-nucleotides - used as PCR primers for producing increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burton DR, Lerner RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q70487 standard; cDNA; 646 BP.
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02-FEB-1993; US-012566.

28-DEC-1993; US-01266.

SOPID SCRIPPS PES INST.

Rarbas CF, Burlon DR, Ler
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Tombinatorial antibody libraries

Example 1: Page 84: 125pp. English

Tis202 and Ti5203 are the heavy and light chain variable domains of a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a Proomb3 can be pression vector. The heavy and light chain variable domains of a seed expression vector. The heavy and light chain variable domains of an entibody library using mutagenic primers. Mutagenic primers of the can antibody library using mutagenic primers. Mutagenic primers of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
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    tycagggccagtcacagtgttagcagggcctacttagcctggtaccagcagaaacctggc 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gageteaggeagtetecaggeaccetgtettgtetecaggggaaagageaccetece 60
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23-OCT-1996 (first entry)
PORAP313 anti-tetanus toxoid Ig light chain variable domain CDNA.
Mutagenesis: Ig: immunoglobulin; FR: framework region: variable; CDR:
complementarity determining region; light; heavy chain; PCR:
polymerase chain reaction; antibody library; diversity; affinity:
immunospecificity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 33; Indels 3; Gaps
                                                                                                                                241 gattttgcagtgtactactgtcagcagtatggtggctcaccgtggttcggccaagggacc 300
                                                                                                                                                                                       238 GATTITGCAGITIATIACIGICAGCAGAGCGIAGCGACIGGGICACITICGGGGGAGGGACC 297
         181 tecaqtggcagtgggtetgggacagaetteaeteteaecateagcagaetggageetgaa 240
                                                              178 Trcagiggcagigggicigggacagacitcacicicaccaicagcaacciagagccigaa 237
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Best Local Similarity 88.6%;
Matches 279, Conservative
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02-SEP-1994; US-300386.
(SCRI ) SCRIPPS RES INST.
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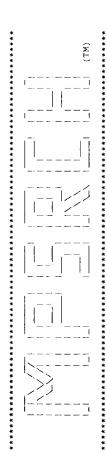
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187 AGIGGGICTGGGACAGACTTCACTCTCACCAACGAACGTAGAGGTTGAAGATTTGGA 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        071872 encodes the light chain of a human type anti-19E peptide of 1872 encodes the light chain of a human type anti-19E peptide monoclonal antibody which inhibits the signal transmission for the release of chemical mediator from mast cells and basophils stimulated with allergen. The antibody can be used for the prophylaxis and the fherapy of allergy. 216 G; 195 T; Sequence 224 BP. 277 C. 216 G; 195 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human monoclonal anti-IqE peptide antibody - inhibits histamine release from mast cells by allergen stimulation, useful for
                                                                                                                                                                                 Human 1gE; CH4 region; triggers mediator release;
Mast cells; Monoclonal antibody; allergy; Immunoglobulin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 924;
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pred, No. 2.08e-135;
                                                                                                                                                 27-ocr-1994 (first entry)
Sequence coding human anti-19E MAb light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kobayashi F, Mizuno A, Morinaga T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= antibody light chain
/note= "Human monoclonal anti-19E antibody
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                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                               071872 standard; cDNA; 924 BP.
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Best Local Similarity 89.0%;
Matches 275; Conservative
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301 aaggtggaactcaaa 315
                         298 AAGGTGGAGATCAAA 312
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07-0CT-1992; JP-2938
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Qy 304 GAGATCAAA 312

Search completed: Tue Feb 24 07:33:58 1998 Job time : 73 secs.

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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Tue Feb 24 13:19:13 1998; MasPar time 215.47 Seconds 866.301 Million cell updates/sec Run on:

not generated. Tabular output

(1-378) from US08844215.sog 378 >US-08-844-215-27 Description:
Perfect Score:
N.A. Sequence:
Comp:

GIGIOGIGACOSTOTCIACA 378 GAGACCAGIGGCACAGAGI 1 GAGGIGCAGCIGGTCGAGIC

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 . . Nmatch STD 665703 seqs, 246912890 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

99:ESTI04 100:ESTI00 101:ESTI01 102:EST102 103:EST103 104:EST104 105:EST105 106:EST105 107:EST107 108:EST106 109:EST109 110:EST110 111:EST111 112:EST112 114:EST113 114:EST113 114:EST113 118:EST113 1

EST-B

Database:

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179.EST179 180.EST180 181.EST181 182.EST182 183.EST183 184.ESS1184 185.EST187 186.EST186 187.ESS1187 188.EST188 189.EST189 190.EST190 191.EST191 192.EST192 193.EST193 194.EST195 196.EST195 196.EST195 196.EST195
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srale 5 289 Variance 1 980; Mean 9.944;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1 (bases 1 to 209)

8 Adams,M.D. Kerlavage,A P., Fleischmann, P.D., Fuldher:P.A., White,O., Sutton.G., Rlake,B.D., Wahite,O., Sutton.G., Rlake,B.D., Wahite,O., Sutton.G., Rlake,B.D., Prichemsnock,K.G., Googane,J.D., White,O., Sutton.G., Rlake,B.D., Prichemsnock,C.D., Geodgane,J.D., Firschend,L.M., FitzHugh,W.M., Fritchomn,J.L., Geodgagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr.P.S., Kelley,J.M., Klimek,K.M., Kelley,J.G., Chiu,L.J., Geodgagen,N.S.M., Meriek,Y.M., Klimek,K.M., Kelley,J.G., Liu,L.J., Geodgagen,N.S.M., Pelley,J.M., Shirlay,P., Small,K.V., Spriggs,T.A., Utterback,T.P., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Utterback,T.P., Saudek,D.M., Shirlay,P., Small,K.V., Spriggs,T.A., Utterback,T.P., Coleman,J.F., Li,Y., Rednarik,D.P., Cao,L., Gepeda,M.A., Collins,E.-J., Dimke,D., Feng,P.P., Ferrie,A., Fischer,J., Hudson,P.P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Melssner,P.S., Olsen,H., Raymon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.G. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon S2 Million Basepairs of CDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).
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                      Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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Pred. No. 8.71e-172;
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
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                                                                                                                                  PEFFRENCE
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1 (Joaces J. Co. Zov.)

2. Adams, M. D. Kerlavage, A. P. Floischmann, P. D. Fuldmer, R.A.,

Rult, C. J. Lee, N. Kirkness, F. E. Weinstnock, K. Gonayno, I. D.,

White, O., Sutton, G., Blake, J. A., Prandon, R.C., Chiu, M. W.

Clayton, P. A. Cline, F. I. Corton, M. D. Earle-Hudwes, J., Fine, L.D.,

FitzGerald, L. M. FitzHugh, W. M. Fritchman J. Gondhagen, N. S.M.,

Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblow, E. Hidkle, IT. P. S.,

Kelley, J. M., Kilmek, K. M., Kelley, J. C., Liu, L. J., Marmaros, S. M.,

Merrick, J. M. Moreop-Palaques, P. F., McPoniald, J. A. Nanyen, D. T.,

Pellegrino, S. M., Phillips, C. A., Pyder, S. E., Scott, J. L.,

Saudek, D.M., Shirley, R., Small, K. V., Spriggs, T. A., Ulterback, T. R.,

Weidman, J. F., Li, Y. Bedacrik, D. P., Cao, L., Copeda, M. A.,

Coleman, T. A., Collins, E. J., Pimke, D., Feng, P., Ferric, A.,

Gruber, J., Hudson, P., Kim, A., Kozak, D. L., Kunsch, C., Ji, H., Li, H.,

Meissner, P. S., Olsen, H., Raymond, L., Wei, Y.-F., Wildow, J., Xu, C.,

Yu, G. L., Ruben, S. M., Dillon, P. J., Fannon, M. P., Rosen, G. A.,
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Eukaryotae; Metazca, Fumetazca, Rilateria; Coelomata;
Deuterostomia, Chordata, Vertebrata, Gnathostomata; Ostejohthyws;
Sarcopterygii, Choanata, Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta, Primates, Catarrhini, Hominidae; Homo.
1 (bases 1 to 287)
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For clone availability, additional sequence and expression
information related to this EST, please contact the TIGK Database
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DEFINITION EST89669 Homo sapiens cDNA 5' end similar to immunoal-dealin heavy
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Homo sapiens
Eukaryotae: Metazoa; Eumetazoa: Bilateria; Coelomata;
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Tel: 3018649056
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Surcopterygil; Choanata; Terrapoda; Amniota; Mammalia; Theria; Butheria; Archonta; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.

Eutheria; M. (230)

Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., Whiteo, S. acton,G. Blake,J.A. Frandon,R.G., Chiu,M.W., Catron,R.A., Cline, R. T. Cotton, M. D., Farle-Huphes, T. Fino,L. D. FitzGerald,L.M., FitzHugh, W. M. Friftchman, I. Googhagen,N.S. M., Relley,J.M., Klimek,K.M., Kelley,J.G., Liu,L.-I., Marmaros,S.M., Mernor-Palanques,R.F., McPonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Fyder,S.E., Scott,J. I. (Special, M. A.)

Saudek,D. M., Shirley,P., Small, K.V., Spriggs,T.A. Unterback,T.P., Weidman,J.E., Li,Y. Pedrarik D.P. Cao, L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Gruber,J., Hudson,P. S., Olsen,H., Raymond,L., Wei,Y. F., Wing,J. Xu,C., Yu,G.T.-L., Ruber,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,M.A., Fields,C., Fraser,C.M. and Venter,J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon S. Million Basepairs of CDNA Sequence
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Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichtbyes:
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932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
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<1..>238
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Fred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.8%;
Best Local Similarity 82.6%;
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Venter, JC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 3018699423
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DEFINITION me87g10 r1 Scares mouse 3NDMS Mus musculus cDNA clone 6,88594 5'
DEFINITION me87g10 r1 Scares mouse 3NDMS Mus musculus cDNA clone 6,88594 5'
Similar to qb:X14584 IG HEAVY CHAIN PPECURSOR V-III PEGION (HUMAN);
qb:V00821 Mouse mRNA fragment for immunoglobulin mu encoding the
of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                        Dukaryotae) Metazoa, Eumetazoa; Bilateria; Coelomata;
Deuterostomia: Chordata: Vertebrata: Gnathostomaia: Ostelchthyes;
Barcopteraygii: Choanata; Tetrapoda: Amniota: Mammalia; Theria;
Butheria: Archorta: Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 385)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Pifkin, L., Pohlfing, T., Sarres, M., Tan, F.,
Trevaskis, E., Materston, R., Williamson, A., Wohldmann, P. and
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 aggtgcaggtngtgcagtctggggctgaagtgaagatgcctgggggcctcagtgaagcttt 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 385;
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0, Mismatches 74, Indels
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Source: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
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Best Local Similarity 69.9%;
Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
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3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M Fatima Ronaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 823)
Marra,M., Hillier,L., Allen,M., Howles,M., Dietrich,N., Eubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 gacgigaagciggiggagictgggggaaggcitagigaagcciggagggicccigaaacic 177
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                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 No 4 220-84:
Mismatches 104,
                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector to vector length is 867
Seg primer: -28Ml3 rev2 from Amersham
High quality sequence stop: 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223
                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson wustl edu
                                                                                                                                                The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="4 weeks"
/lab_host="DH10B"
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Best Local Similarity 63.3%;
Matches 183; Conservative
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3 298 €
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                                                                                                                            Waterston, R.
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RESULT

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Vertebrata; Butheria; Artiodactýla; Suiformes; Suina; Suidae; Sus.
1. (bases 1 to 330)
                                                                                                                                                                                                                                    Winteroe, A.K., Fredholm, M. and Davies, W. Evaluation and characterization of a porcine small intestine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 similar to the MCG726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="small intestine"
/clone_lib="directionally cloned cDNA in XL1-blue MRF''
/clone="cld10"
                                                                                                                                                                                                                                                                                                                                                                               Submitted (26-JUL-1995) Winterow A K., The Royal Veterinary and Agricultural University, Department of Animal Science and Animal Health, Division of Animal Genetics, Bulcwsvej 13, 1870 Frederiksberg C, DENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 gaggagaaggtggtggagtetqgaggaggeetggtgeagnetggggnggtetetetaaqaete 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 ccagggaaggggctggagtggctggcggctattagtactagtcytggtagtactactactac 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GCTGGACAAGGTGTTGAGTGGATGAGGAATGATGATGATGATGATAAGTAGGAAACTAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GCACAGAAGITTCAGGGGCAGAGTCACAATTACCCGGAACAAATGCACGGCCACAGGCTAC
                                                                                     diversity region: EST; expressed sequence tag; immunoalobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 tootgigtoggotolggalloacolloagidgiacolanaljaacigdgirodcoaddol 177
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                                                                                                              immunoglobulin heavy chain; joining region; variable region.
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                          clone cldlu).
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IG HEAVY CHAIN V-III REGION (HUMAN);.
                        S serofa mRNA: expressed sequence tad (57
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                                                                                                                                                                                                                                                                                                  Genome 7, 509-517 (1996)
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I and cloned into the Pac I and Ecc PI sites of the modified pi7f?
                                                                                                 Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes, Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria, Butheria, Archenta, Primates, Catarihini, Hominidae, Homo.

Hillier.L., Clark, N., Dubuque, T., Fliston, K., Hawkins, M., Hultan, M., Kucoba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Fiftin, L., Pohlfing, T., Sarres, M., Tan, F., Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 TGTTGGSAACARTAAGTAGGCAGARARTTTCARREGERASAGTCACAATTAGGGSAGG 220
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                    Library went through bne reduced of normalization.
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                                                                                   Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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                                           constructed by Bento Scares and M.Fatima Bonaldo.
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Washington University School of Medicine
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/clone="214441"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson wustl edu
High quality sequence stops: 261
Source: IMAGE Consortium, LLNL
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Local Similarity 61.8%;
nes 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                 Homo sapiens
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double-stranded oppNA was ligated to Ev. 81 adaptors (Pharmacia), digasted with Not 1 and cloned into the Not 1 and Foo RI sites of modified pr713 vector (Pharmacia). Library went through one round of normalization to a Chermacia, Eibrary constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                          Desterostomia, Cherdata, Vertebrata, Snathostomata, Osteichthyes, Sarcopterggii, Choanata, Tetrapoda: Anniota, Mammalia; Theria: Eutheria: Archonta; Primales; Catarrhini; Hominidae; Homo (bases 1 to 430)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Kucaba, T., Elliston, K., Hawkins, M., Ruchan, M., Kucaba, T., Sares, W., Tan, F., Tan, F., Tan, F., Tan, F., Tan, F., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                      Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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Source: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tral: 314 285 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-Merck EST Project
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Location/Qualifiers
                                                                                                                                                                                                                                                                               The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
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              and M Fatima Ronaldo.
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                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson PK
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                   Homo sapiens
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⊖(
Sarcopterydii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhin; Hominidae; Home; 1 (Dases I to 297)

1 (Dases I to 297)

2 Adams, M. N. Kerlavare, A.P., Fleischmann, P. D., Fuldner, P. A., Brandon, R.C., Chiu, M. W., V., Clayton, P. A., Cilne, P. T., Cotton, M. D., Earle-Hughes, T. Fine, I. D., FitzGerald, L. M., FitzHugh, W. M., Fritchman, T. L., Geoghagen, N. S. M., Glodek, A., Gohem, C. L., Hanna, M. C., Hedblom, F. S., Glodek, A., Gohem, C. L., Hanna, M. C., Hedblom, S. M., Moreno-Palanques, P. F., Morbonald, L. A., Naysen, D. T., Pelley, J. M., Moreno-Palanques, P. F., Morbonald, L. A., Naysen, D. T., Pelley, J. M., Shirley, R., Saudek, D.M., Shirley, R., Sandlik, V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D. P., Cao, I., Cepeda, M. A., Collans, E. J., Shirley, R., Sirley, R., Feng, P., Ferrie, A., Fischer, C., Hastings, G. A., He, W. Hu, T. S., Greene, T. M., Li, M. Meisner, P. S., Olsen, H., Paymond, L., Weil, Y. S., Greene, T. M., Hasting, G. A., Millon, P. J., Fannon, M. P., Rosen, C. A., Haseline, M. A., Fields, C., Fraser, C.M., and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of CDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tdbinfoetdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Venter, JC
The Institute for Genomic Research
93z Clopper Rd, Gaithersburg, MD 20
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"<11..>297
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Best Local Similarity 66.0%;
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modified pTTT3 vector (Pharmacia). Library went through one round of normalization to a Cot - 20. Library constructed by Bento Soares
Eskaryotae, Metazoa, Eumetazoa, Bilateria, Coelomata.
Deuterostomia, Chordata: Vortebrata; Gnathostomota: osteichthyos;
Sarospierydii: Choquata; Tetrapoda; Amtiota: Mammalia, Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H43753 478 bp mRNA EST 41-JUL-1995
yp21g51 r1 Home Sapiens CDNA close 188112 f1 similur to abil24556
IG HEAVY CHAIN V-11 REGION (HUMAN);.
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Deuterostomia: Chordata, Vertebrata; Gnathostomata; Osteichthyes:
Sarcopterygli: Choanata; Tetrapoda: Amniota; Mammalia: Theria:
Eutheria: Archonta; Primates; Catarrhini: Hominidae; Homo.
1 (bases 1 to 478)
Hillier.t., Clark,N., Dubuque,T., Elliston.K., Huwkins,M.,
Hillier.t., Glark,N., Ku, aba,T., Ic.M., Ichnon,G., Marra,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL.
This clone is available royally-free through LLNL.; contact the IMAGE Consortium, (anto-finally-free through LLNL); contact the IMAGE Consortium, (anto-finally-free considered overall poor quality.
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                                                                                      Washington University School of Medicine
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Best Local Similarity 68:09, Pred, No. 1.896 42;
Matches 66; Conservative 0; Mismatches 11; Indels
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Eukaryotae, Metazoa: Eumetazoa: Bilateria: Coelomata:
Eukaryotae, Metazoa: Eumetazoa: Bilateria: Coelomata: Strichthyes:
Deuterostomia: Chordata: Vertebrata: Gnathcatomata: Theria.
Bartheria: Archonta: Primates: Catarrhini; Hominidae: Homo

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4444 Forest Park Parkway, Box 85N1, St. Louis, Mp 53108
Tel: 314 286 1810
Fax: 314 286 1810
Parsons,J., Rifkin,L., Rohlfing,T., Scares,M., Tan,F.,
Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P.
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                                                                                                                              The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                 For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).
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4444 Pornst Park Parkway, Ph.8 8501, St. Louis, MO 63108
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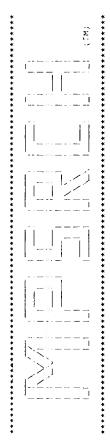
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Eukaryotae; Metazoa; Eumetazoa, Bilateria; Coelomata; Deuterostomia; Chordata: Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygli; Choanata: Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhid; Hominidae; Homo. 1 (bases 1 to 303) Hillier, C., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Bitkin, L., Rohlfing, T., Waterston, R., Wohldmann, P. and
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IG HEAVY CHAIN V-III REGION (HUMAN);
                                      High qality sequence stops: 139 Source: IMAGE Consortium, LLNL
This clone is available ropalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Park Parkway, Box 8501. St. Louis. MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                       0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                            Score 39; DB 4; Length 169;
Pred No. 7,40e-32;
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                                                                                                                              Location/Qualifiers
               Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
Fax: 314 286 1810
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/organism="Homo sapiens"/clone="187156"

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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT713 vector (Pharmacia), Library went through one round of accmalication to a fort \sim 20 library constructed by Wento Soares
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This clone is available royalty free through LLNL. contact the IMAGE Consortium (informage.ilml.gov) for further information.
                                                                                                                                                                                                                                                                                            112 ayatgcayotayaayaytotyayyyaayaqaytgatoraaqootgayaaqayoortot 171
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Farsons,J., Rifkin,L., Nohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                              Length 403;
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Pred. No. 4.46e-25;
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Washington University School of Medicine
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                                                                                                                              Score 39;
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    91.
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nes 89; Conservative
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Fax: 314 286 1810
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Release 2.1D John F. Collins. Biocomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Fob 24 07 07 16 1998, Maspar time 6.87 seconds 266 870 Million cell updates/sec Publich

Tabular output not generated.

>US-08-844-215-1 (1-132) from US08844215.pcp 956 1 EVOLLEQSGAEVRREGSSVK......RCYPGFPQQWGGGILVTVSS 132 Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

111726 segs, 13889129 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq30 Database:

lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10.part10 11.part11 12:part13:part13
14.part14 15:part15 16 part16 17 part17 18:part18
19:fart19 20.part20 21.fart21 12.fart22 23:part23

Mean 30.954; Variance 153.540; scale 0.202 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		Ouerv					
NO.	Score	Match	Match Length DB	DB	ID	Description	Pred. No.
	0	Ci.	- σο	5	R24442	Sequence of antibody	1.37e-47
C1	U)	58.5	120	ch	R54795	SpA-reactive IqM heav	4.30e-36
٣	557	58.3	476	9	R31023	eavy	6.32e-36
4	549	7	123	<u>رم</u>	W19888	CEA-specific antibody	2.94e-35
S	537	φ	86	12	R72058	VH region.	.94e-3
9	534	v.	123	C1	WIGRET	CEA-specific antibody	5.230-34
7	533	5.	123	C)	W19889	CEA-specific antibody	6.34e-34
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11	526	יא ניש	-112	( ·	W13536	Anti-melanoma antibod	
15	527	₹.			545610	Monoclonal antibody G	~
13	515	m		- 1	690244	HV126? VH region.	.03e-3
14	515	'n			R22358	Protein encoded by th	2.00e-32
15	515	m.			R38623	Human heavy chain V r	.00e-
16	515			50	W03950	DNA fragment vh49 8,	2 000-32
17	515			-1	P75964	HSV-neutralising anti	.33e.
18	513	ω.		œ,	P54795	SpA-reactive 1gm heav	2 936-32
σi	C4 65	65	; ;	• •	P11814	Biranised mouse DRO-2	3 146-31
0.2	C1	53.6	C # C	σ,	75554	DPEG-200 Humanired an	3 546-32

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anti-tumour. ised heavy ch chain mariab ised 561 1 vH	cary chair caracter consists of the house antibody but hoavy chair rariably umanised Cop-graft.	1864 CDP-37ATT 1864 5G1.1 VH 1864 C4G1 19 H 1864 C4G1 19 H	uman hum nise reg reg	3/Humanised heav 74RPHC VH region 3/Humanised heav 748RHA VH region. anised M291 antib
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AQNYAQKFRDRVSIIADESTSTIELSNLRSDDTAVYYCARDPPRYCSAGRCYPGFFQQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A B-cell superantigen (349) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The SAG is used to enhance production of VH, especially VH3, restricted Abs. During attempts to identify sAGs, as sequences (R54784-801) of H chains from Ig reactive with mod-SpA, and as and DNA sequences (R54802-16, G6482-56, of VH regions of SpA binders obtained from combinatorial libraries were determined. IgM protein RAS is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 vhlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifg--g- 56
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                                                                                                                                                                                                                                                                                                                                                             84 yaq----kfqgrvtltadeststaymelsslrsedtavyycardngaycsggscysgwfd 139
                                                                                                                                                                                                                                                                                                                                                                                    61 YAQNYAQKFRDRVSIIADESTSTSFIELSNLRSDDTAVYYCARDPPRYCSAGRCYPGFFG 120
additional N-linked qlycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding ability. They are preferably located in the CH2 region of the Iq molecule. Antibodies bearing multiple sialyl-Lex determinants are useful for disrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury. Sequence 481 AA:
                                                                                                                                                                                                                                                                              qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtan 83
                                                                                                                                                                                                                                                                                                                  1 EVOLLEQSGAEVRRPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIPIFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spa-reactive 1gM heavy chain clone KAS.
SpA domain D; Ig binding region; 1gM; B-cell superantigen; sAg;
superantigen; heavy chain variable region; VH3 restricted antibody;
VH; protein-A; KAS; B-lymphocyte; vaccine.
                                                                                                                                                                                                                                        5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 94-167127/20.
Stimulating prodn. of variable region gene family restricted
antibodies - through B-cell super-antigen vaccination
Disclosure; Fage 78; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 58.5%; Score 559; DB 9; Length 120; Local Similarity 68.7%; Pred. No. 4.30e-36; os 90; Conservative 16; Mismatches 14; Indels 1
                                                                                                                                                                                           Score 696; DB 5; Length 481; Pred. No. 1.37e-47;
                                                                                                                                                                                                                                      16; Mismatches 12; Indels
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P54796 standard: peptide: 120 AA
                                                                                                                                                                                                 72.8%;
Local Similarity 75.0%;
hes 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 wqqqtlvtvss 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 OWGQGTLVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 pwgqgtlvtvss 151
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29-OCT-1993; U10555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-0CT-1992;
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Disclosure: Fig 2: 35pp; English.

The sequence given in Kil023-24 represent the heavy and light chaims. The sequences given in Kil023-24 represent the heavy and light chains of Antibody D is a monoclonal antibody Which of Antibody D is closely related in nature (HMV) sero positive patient. Antibody D is closely related in nature of murine antibody BBB3. Total RNA was sisolated from antibody D beaverssing cells and polydemylated RNA was extracted. These polyARN's were used to prepare a cDNA library which was screened for human Rappa light (L) chains and two positive clones were detected. Sequence 476 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 ysqnf-q---grvtitadkststahmeltsirsedtavyycatdryrqanidrarvqwid 144 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:11 | 1:
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                                                                                                 blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prodn. of recombinant primate antibodies - useful for treating
infections caused by hepatitis A, B and C, herpes,
cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
                                                                                        Heavy: light, chain: antibody; D: monoclonal; peripheral; blood
Hymphocyte; hepatitis A virus; HAV; sero; positive; patient:
murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 476;
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Pred. No. 6.32e-36;
                                                                                                                                                                                                              Location/Qualifiers
AA.
R31023 standard; Protein; 476
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tes 85; Conserved
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(WELL ) WELLCOME FOUND LTD.
                                                   19-MAY-1993 (first entry)
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15-JUL-1991; GB-015284.
                                                                                                                                                                                                                                                                  "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85..113
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                                                                                Antibody D heavy chain
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                                                                                                                                                                                                                                                                                                                                                                            /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR2
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                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                             'note=
                                     R31023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This polypeptide sequence comprises the heavy chain variable region (VH), Habli, obtained by mutagenesis of the VH CDR's fhuman article sequence comprises the heavy chain variable region (VH), Habli, obtained by mutagenesis of the VH CDR's fhuman carcinoembryonic antipen (hCBA) specific antibody CEA6 (see W19881). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 cextracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W1987-65), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. An example of a claimed pairing is HBB11 VH with CEA6 VL. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer of a gament of the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 yaq----kfqgrltitadeststaymelsslrsedtavyycarhnhny-el-yyy--ymd 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YAQNYAQKFPDFVSITADESTSTSFIELSNLPSDDTAVYYGAPDPPPYGSAGPCYPGFFQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 qvqlv-qsgaevkkpgssvkvsckasggtfsnspinwlrqapggglewmgsiipsfgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLLEQSGAEVPKPGSSVKVSCKASGGTFSGHVITWVRQAPGGGLEWMGESIPIFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Specific binding members for human carcinoembryonic antigon · bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells, used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 57.4%; Score 549; DB 23; Length 123; Local Similarity 66 7%; Prod No 2.94e-35; nes 88; Conservative 16; Mismatches 19; Indels
                                                                                                         07-0FC-1997 (first entry)
CEA-specific antibody CEA6 VH mutant HBB11 sequence.
Carcinoembryonic antigen: CEA: human: antibody: scFv;
tumour marker: lung cancer; breast cancer; colon cancer;
adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                       /note- "complementarity determining region 1"
Region
                                                                                                                                                                                                                                                                                                                       "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osbourn JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                           Location/Qualifiers
                                                              T 4
W19888 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCafferty JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                  11-057-1996; GP-021295.
07-DEG-1995; GR-025904.
23-MAY-1996; GB-010824.
                                                                                                                                                                                            Chimeric Homo sapiens;
             121 SWGGGTLVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 vwqqqtmvtvss 123
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                                                                                                                                                                                                                                                                                                                                                                                                                      09-DEC-1996; G03043.
                                                                                                                                                                                                          Chimeric synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 97-319779/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AA;
W09720932-A1.
                                                                                                                                                                                                                                                                                                        /label- CDR2
                                                                                                                                                                                                                                                          /label- CDR1
                                                                                                                                                                                                                                                                                                                                                       /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allen DJ,
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                                                                                             W19888;
                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                            Region
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1 qvqlv·qsgaevkkpgssvkvsckasgqtfssyaiswvrqapgqqlewmggiipifgtan 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 537, EB 12, Length 98;
Pred. No. 2.94e-34;
13; Mismatches 6; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Graves' cphthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCR bisclosure; Page 88; 94pp; English.

L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (1961) genes showed homology to the closest germline genes, DF12 (202127) and PRIZOR (SP3228). The DNA (2003229) and corresp. amino acid (PRIZOR) sequences of the VH region of a representative clone, Sequence. 98 AA;
                                                                                                                                                     Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W19881;
07-DEC-1997 (first entry)
CEA-specific antibody CEA6 VH sequence.
Carcinocmbryonic antigen; CEA; human; antibody; scFv;
tumour marker, lung cancer, breast cancer, colon cancer;
adenocarcinoma; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "complementarity determining region 1"
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Pegion 99.112
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11-077-1966; GR-021295.
07-DEC-1995; GR-025004.
23-MAY-1995; GR-010824.
(CAME-) CAMBRIDGE ANTIRODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 31...35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-1995.
22-SEP-1994; U10756.
22-SEP-1993; US-124469.
(NICH-) NICHOLS INST DIAGNOSTICS.
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R72068 standard; Protein; 98 AA.
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Best Local Similarity 76.7%;
Matches 79; Conservative
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mclachian SM, Rapoport B;
WPI; 95-139383/18.
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                                                                          26-SEP-1995 (
DP10 VH region
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                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CDR2
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/label= CDR1
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09-DEC-1996,
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Allen PJ,
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                                                                                                                                                                                                                                                                                                                                                           4atches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gvqlv-qsgaevkkpgssvkvsckasggtfsnspinwlrqapgqglewmgsiipsfgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLLEQSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIPIFGSAN 60
                                                                                                                                                                            A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                             Specific binding members for human carcinoembryonic antigen · bind to the A3-B3 extracellular domain of hCEA and are substantially
                                                                                                                                                                                                                                                                       sequences from training of the properties of a well as CEA6 VH and VL variants, including combinations of CEA6 VH with VL regions from CEA6, ToROA2, TOROAS, TOROAS, LORDIS, LORDIS, LORDIS OF A LOSTS.

(A) is used to detect cells expressing hoEA, in vivo or in vitro, especially tumour cells for diagnossing cancer, e.g. adenocarcinoma
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                                                                                                            This polypeptide sequence comprises the heavy chain variable region (VH) of human carcinoembryonic antigen (hCEA) specific antibody CEA6 VH (T72126-32) and VL (T7213-33) gone segmences were obtained for anti-hCEA antibodies CEA1-CEA7 (see W19876-85).
                                                             non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                         / match 55.9%; Score 534; DB 23; Length 123;
Local Similarity 65.9%; Pred. No. 5.23e-34;
Hes 87; Conservative 77.
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CEA-specific antibody CEAA VH mutant HBBK sequence
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                                                                                              Claim 4; Fig la; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                           the colon, lung or breast.
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97-319779/29
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07-DEC-1995; GB-025004.
23-MAY-1996; GB-010824.
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WPI; 97-319779/29.
                                                                                                                                                                                                                                                                                                                                                                           123 AA;
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               N-PSDB;
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Matches
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This polypeptide sequence comprises the heavy chain variable region (VH), HBB5, obtained by mutagenesis of the VH ChR3 of human carcinomehryonic antigen (hCBA) specific antibody CEAG (see W1988). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation of constant for hCBA of less than 1 x 10 - 8 M, is non-cross-rearrive with human liver cells, and preferrentially binds to the A3.8 sectionally of hCEA and/or to cell-associated hCEA over the A3.8 sectional domain of hCEA and/or to cell-associated hCEA over soluble hCEA, Preferred (A) include pairings of the A3.8 section CEA1-2 (see W19876.85), or their CDR sequences as well as CEA6.9 W with CEA6.9. An example of a claimed by mutagenesis or chain shuffling. An example of a claimed by the CEA6, in vivo or in vitro, especially tumour cells for diagnosing cancer e g adenorarcingma of the colon lung or breast.
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This polypeptide sequence comprises the heavy chain variable region
(VH), HBA11, obtained by mutagenesis of the VH CDR3 of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wri: 97-319779/29.
Specific binding members for human carcinoemblyonic antigen - bind
to the A3-B3 extracellular domain of hCEA and are substantially
non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12:
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tumour marker; lung cancer; breast cancer; colon cancer;
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Pred. No. 6.34e-34;
17; Mismatches 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //note= "complementarity determining region 1"
Region
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W19887 standard; Protein; 123 AA.
                                                                                      Ciaim 4; Fig 2; 128pp; English.
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Best Local Similarity 65.9%;
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23-MAY-1996; GB-010824.
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Chimeric synthetic
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Pred. No. 7 58e-34;
19; Mismatches 17; Indels 9; Gaps
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carcinoembryonic antiqen (hZEA)-specific antibody CEA6 (see N19881). "A claimed specific binding-member (A) comprises an hCEA specific antibody antiqen binding-domain that has a dissociation constant for hCEA of less than 1 x 10 - M is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over acluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1- (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W1986-55) obtained by mutaquenes; or chain shuffling. (A) is used to detect cells expressing hCEA, in vivo or in vivro, especially tumour cells for diagnosing cancer, e.g. adenocarrinoma of the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 4; Fig 2; 128pp; English.

This polypeptide sequence comprises the heavy chain variable region (VH), ToEDIO, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antiqon (ACEA) specific antibody CEA6 (see W1981). A claimed specific binding member (A) comprises an HCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 - 8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Specific binding members for human carcingembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells, used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carcincombryonic antigen: GEA; human; antibody; soPv;
tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1997 (first entry)
CEA-specific antibody CEA6 VH mutant T06D10 sequence.
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50, 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CAMB-) CAMBRIDGE ANTIRODY TECHNOLOGY Allen DJ, McCafferty JG. Osbourn JK.
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W19996 standard, Protein, 123 AA.
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Best Local Similarity 65.9%;
Matches 87; Conservative
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07-DEC-1995; GR-025004.
23-MAY-1996; GR-010824.
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09-DEC-1996; G03043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= CDR1
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                                                                                                                                                                                                                                                          Sequence
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61 YAQNYAQKEFDRVSIIADESISISEIELSNLPSUDIAVYYGAPUFFRYGSAGRCYPGFF© 120
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A human anti-Variceala zoster virus monoclonal antibody was prepd.
using the tricma method of Ostborg ot al. (1983) Hybridoma 2.461-367.
One resultant trioma neutralised VZV in the absence of complement.
This cell line, designated cell line 1C95RAP, produced an antibody designated 93RAP or the light and heavy chain variable region penes of the 93RAP antibody were cloned using PCP. At least two heavy chain (gamma-1) and two light chain (kappa) specific clones sequence (300 082749 $ Q82750 respectively).
                                                                                                                                                                                                                                                  1 qvqlv-qsqaevkkpgssvkvsckasgqtfsnspinwlrqapgqqlewmgsiipsfqtan 59
                                                                                                                                                                                                                                                                                     1 EVQLLEQSGAEVPKPGSSVKVSGKASGG1FSGHVITWVPGAPGGLEWMGF51P1FGSAN 60
hdEA over soluble hdEA. Freferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA5 VH and VL variants (see W1986-95) obtained by mutagenesis or chain shuffling. Examples of claimed pairings are TC5D10 VH with TC5D12 or CEA6 VL. (A) is used to detect cells expressing hdEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
                                                                                                                                                                                                            9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Varicella coster virus: VZW, anti-VZW meneclenal antibody, 99KA9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93KA9 anti-Varicella zoster virus antibody heavy chain variable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human monoclonal antibodies specific for the glyco:protein II
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                                                                                                                                                                   Score 530; DB 23; Length 123:
Pred. No. 1.13e-33;
                                                                                                                                                                                                              17; Mismatches 19; Indels
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                                                                                                                                                                         Query Match
Best Local Similarity 65.9%;
Matches 87; Conservative
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/label= mature light chain segion
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                                                                                                                                     123 AA;
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24-MAR-1994;
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/label= CDR
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                                                                                                                                       Sequence
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Match 55.3%; Score 529; DB 12; Length 147; Local Similarity 64.2%; Pred. No. 1.37e-33; Score 20; Mismatches 20; Indels 9; Gaps es 86; Conservative 20; Mismatches 20; Indels 9; Gaps

Query Match

Matches

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20 gygly-gsgaevkkpgssykysckasggtfsnfaiswyrgapggglewmgrimplfyts- 77

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Taim 19; Page 75-76; 82pp; English.

A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphocytes to the page library in a binding assay with cultured tumour cells of the same type as the patient; (b) screening for anti-tumour antibodies in thype as the patient's tumour; (c) removing extraneous antibodies by absorption against normal human cells. (d) cloning the phage selected in step (b) and (c); (e) assaying the specificity of the cloned phage by incubating the phage with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phage that do not bind continued tumour cells derived from more than one other tumour that is not the patient's tumour. The present sequence represents a human heavy chain antibody, from a VH antibody fusion phage library, produced by a method as described above. The antibodies produced can be used for the human antibody studies and for isolating tumour may be human and for isolating tumour may be human antibodies to studying tumour patient's the patient's the antibodies produced can be used for the human antibodies to studying tumour may an incompany the second continued to the human antibodies produced can be used for the human antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine monoclonal antibodies (MAbs). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a tumour cell line can be improved by genetic manipulations.
                                                78 -t--yaqkfqgrvtisadaststaymelsslrsddtamyycardita-pgaaptplnfyg 133
                                                                            1 EVOLLEGSGAEVPKPGSSVKVSCKASGGTESGHVITWVRQAPGGGLEWMGESIPIFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 SGAEVRKPGSSVKVSCKASGGIFSCHVITWVRQAPGQGLEWMGESIPIFGSANYAQNYAQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 gglevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtanyaq---- 62
                                                                                                                                                                                                                                                                                                                                                 28-0CT-1997 (first entry)
Anti-melanoma antibody 2-71 from VH antibody fusion phage library.
Human: monoclonal antitumour antibody; peripheral blood lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodn. of human monoclonal anti-tumour antibodies - by screening a fusion phage library produced using peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The human antibodies have low immunogenicity in humans compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 55.0%; Score 526; DB 23, Length 119.
Best Local Similarity 69.6%; Pred No 2 43e-33;
Matches 87; Conservative 16; Mismatches 10; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                     tumourigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                        W13536 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID • R45610 standard; Protein; 124 AA. AC PW5610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-1996, IB1032,
30-JUN-1995, US-497647.
(UYYA.) UNIV YALE.
Cal X., Garen A:
                                                                                                                                                     134 mdvwgqgttvtvss 147
                                                                                                                                                                                                   120 00-WGOGTLVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from a cancer patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 VTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09702479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-1997
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60 ysqnf-q---grvtltadeststvymelsgltsadtavyycaksqaqwsnlirs-p--id 112
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                                                                                                                                                                                                                                                                                                                                                                             unca tautovige sactimes.
Claim 6: Page 20-23: 34pp; English.
The monoclonal antibodies (MAb's) designated GP13, GP44 and GP68
react with HIV-1 gp120 giyopotein variants containing the amino-
acids Asn88. Lys17, Asn262 and Tyr 435 but exhibit at loss forware reacced reaction with gp120 variants in which those amino acids have been deleted or substituted. The MAb's are useful to passive immunotherapy and their anti-idiotypic antibodies can be useful in the production of vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gvglv-gsgaevkkpgssvkvsckasggtfssstlnwvrgtpggglewmakilptluss! 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLLEQSGAEVHKPGSSVKVSCKASGGTFSGHVITWVÞGAPGGGTFWMGFGTUTFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seps
                                                                                                                                                                                                                                                                                                                                  Monoclonal antibodies to HIV-1 - directed against glycosprotein
gpl20, useful for passive immunotherapy or prodn. of
anti-idiotype vaccines
22-JUL-1994 (first entry)
Monocolonal antibody GP68 heavy chain (V H I).
Muncolonel antibody GP68 heavy chain (V H I).
ervelope monocoficiency Virus; gp120; glycoprotein:
ervelope protein, mangalenal antibody MAb: vaccine; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Graves ophthálmopathy associated immunoglobulin protein:
orbital antigen; monoclonal antibody: heavy chain; H chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 521; DB 9; Length 124; Pred. No. 6.32e-33; 19; Mismatches 22; Indels
                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
31..35
                                                                                                                                                                                                   /label- Framework IV. JH4 segment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-1994; U10756.
22-SEP-1993; US-124469.
(NICH-) NICHOLS INST DIAGNOSTICS.
Mclachlan SM. Rapoport B;
                                                                                                                                                                                                                                                                               (NEWE-) NEDERLANDEN. MIN WELZIJN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R72069 standard; Protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.5%;
62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 52.54.
83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-1995 (first entry)
                                                                                                                                                                                      111..124
                                                                                                                                                         99..110
                                                                                            31..35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 QWGQGTLVTVSS 132
                                                                                                                                                                                                                                                 05-JUL-1993; 201959.
                                                                                                                                                                                                                                                                                               Osterhaus ADME;
WPI; 94-036603/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95-139383/18
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                                                                                                                                                                                                                                                                                                                           N-PSDB; 055663
                                                                                                                                        /label= CDR 2.
                                                                                                                                                                      /label= CDR 3.
                                                                                                          'label CDR 1
                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- CDR1
                                                                                                                                                                                                                                    02-FEB-1994.
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30-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                             Region
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Scarch completed: The Pab 24 07:03:57 1098 Job time : 41 secs.
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                                                                                                                                                                                                                                                                                                                                                          20 gvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggqlewmgriipilg-i- 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLLEQSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGFSIPIFGSAN 60
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                                                                                                                                                                                                                                                                                              5, Gaps
                               by molecular cloning of immunoglobulin genes by PCR I become to the base of 94pp. English.

1. and H-chain DNA was amplified by PCR from Graves' orbital tissue and chones encoding auroimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (IGG1) genes showed homology to the DNA (089329) and corresp. DP10 (089327) and hv1262 (089328). The DNA (089329) and corresp. DP10 (089327) and CP7H1.2, are provided.

Sequence 98 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector lambda FIX II was screened with the human VHI family specific oligonucleotide (see Q22418). Phage clone lambda 49.8 was isolated and a 6.1 kb Xbai fragment congo. the variable segment VH49.8 subcloned into pNU3 to generate plasmid pVH49.8. An 800 bp region of this insert was sequenced. VH49.8 was found to have an open reading frame which encoded the sequence shown.
                  ' ophthalmopathy-associated monoclonal antibody - produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENP.) GENPHARM INT INC.
Lonberg N. Kay R.
WPI. 92-113-92-113-12-144.
Immunoglobulin trans:genes - for prodn. of heterologous non-rearranged and/or rearranged in chains.
Example 14: Page 87: 172pp. English.
The human placental genomic DNA library cloned into the phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-1992 (first entry)
Protein encoded by the human heavy chain V region gene VH49.8.
Heavy chain: variable region; VH1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 515; DB 4; Length 117; Pred. No. 2.00e-32;
                                                                                                                                                                                                                                                  Score 515, DB 12, Length 98;
Pred. No. 2.00e-32;
                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1993 (first entry)
Human heavy chain V region VH49.8.
Immunoglobulin: IgG; heavy chain; minilocus transgene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 YAQNYAQKERDEVSIIADESTSTSFIELSNIPSDOTAVYYJAP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 -a-nyaqkfqgrvtitadkststaymelsslrsedtavyycar 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YAQNYAQKFRDRVSIIADESTSTSFIELSNLRSDDTAVYYCAR 103
                                                                                                                                                                                                                                                                                                                                                                                                                58 -a-nyaqkfqgrvtitadkststaymelsslrsedtavyycar 98
                                                                                                                                                                                                                                                                                            13, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R22358 standard; Protein; 117 AA R22358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R38623 standard; Protein; 117 AA
                                                                                                                                                                                                                                                    / Match 53.9%;
Local Similarity 74.8%;
nes 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 53.9%;
Best Local Similarity 74.8%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1992.
28-AUG-1991; UO6185.
29-AUG-1990; US-574748.
31-AUG-1990; US-575962
N-PSDB; 089328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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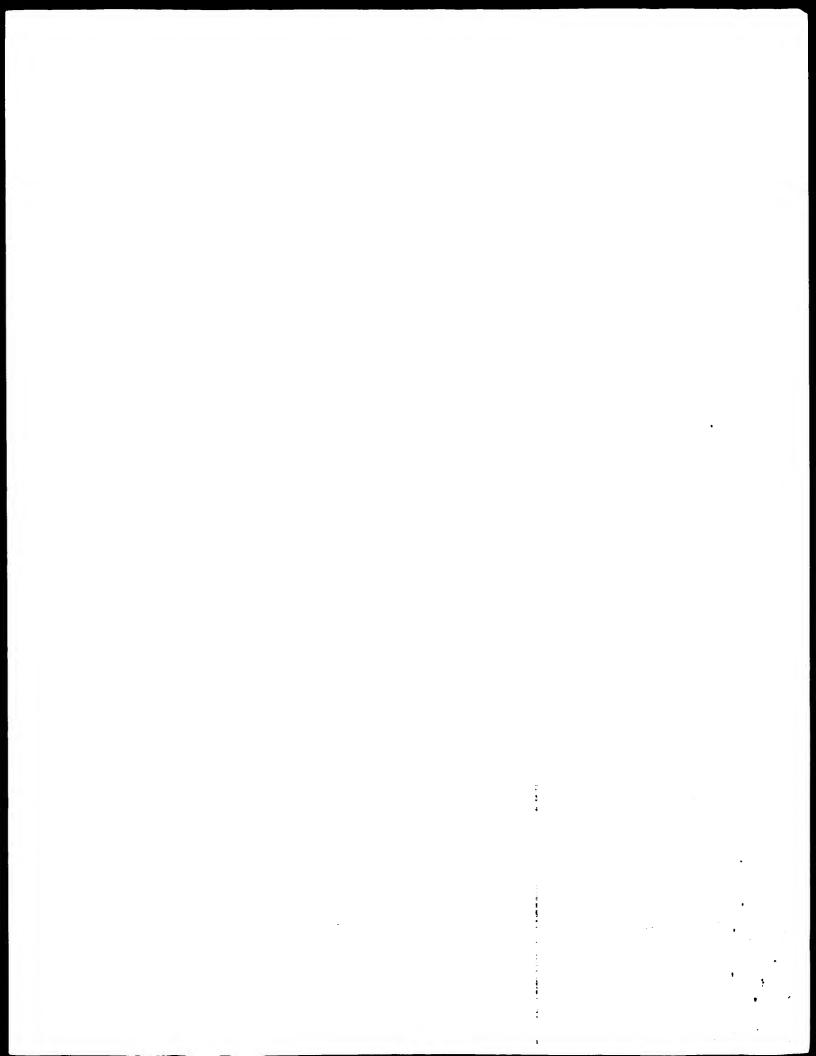
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Example 12, Fage 96, 196pp, English.

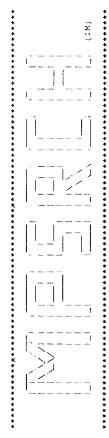
A human placental genomic DNA library cloned into the phage vector lambda FIX II was screened with the human VH1 family specific oligonucleotide Q44184. Phage clone lambda 49.8 was isolated and a fib Xbal fragment containing the variable, segment VH49.8 was subcloned into pNNO3 to generate plasmid pVH49.8 An 800bp region of this insert was sequenced (Q44185) and VH49.8 found to have an open reading frame and inteat splicing and recombination signals, indicating that the gene is functional. Amino acid sequence Q44185 was deduced from the coding sequence; the last 3
                                                                                                                                                                                                                              Transgenic non-human animals contg. immunoglobulin heavy chain trans gene . used to produce useful antibodies by isotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codons before the termination codon have not been translated. Sequence 117 AA;
sotype switching; H chain variable region.
                                                                                                                                                      (GENP-) GENPHAPM INT INC.
                                                                         17-DEC-1992; U10983.
17-DEC-1991; US-810279.
18-MAR-1992; US-853408.
                                                                                                                                    23-JUN-1992; US-904068
                                                                                                                                                                           Lonberg N;
                                                                                                                                                                                         WPI: 93-214169/26.
                                                                                                                                                                                                              N-PSDB; Q44185.
                    Homo sapiens.
                                                       24-JUN-1993.
                                                                                                                                                                                                                                                                         switching
                                                                                                                                                                           Kay RM,
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20 qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmgriipilg-i- 76 1 EVOLLEUSGAEVRKPGSSVKVSCKASGGIFSGHVITWVRQAPGOGLEWMGESTPTFGSAN 60 61 YAQNYAQFFPOPVSJIADESISTSFIELSNIPSDDTAVYYGAP 103 77 -a-nyaqkfqgrvtitadkststaymelsslrsedtavyycar 117 CD Ö

5, Gaps

Query Match 53.9%; Score 515; DB 7; Length 117; Best Local Similarity 74.8%; Pred. No. 2.00e-32; Matches 77; Conservative 13, Mismatches 8, Indels





Pelease 2.15 John P. Collins, Biocomputing Pesearch Unit. Copyright (c) 1992, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Peb 24 07:31-49 1998; MasPar time 2.19 Seconds 210.908 Million cell updates/sec Run on:

Tabular output not generated.

(1-132) from US08844215.pep 956 >US-08-844-215-1 Description: Perfect Score:

RCYPGFFQQWGQGTLVIVSS 132 1 EVQLLEQSGAEVRKPGSSVK Sequence:

PAM 150 Gap 11 Scoring table.

56402 segs, 5095871 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued libackl 2.51 3.52 4.53 5.54 6.55 7.56 8 priso a priso l0.priso 11.priso 12.prist 13 priso 14.priso

Mean 28.505; Variance 140 983; scale 0.203 Statisties.

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		æ					
Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
-	. 0	3.	( C)			Sequence 45, Applicati	4.3
C1	C)	CC L	C1		-58652-	C.	σ
m	539		130	덛	PCT-US93-1	12, Applica	Τ.
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10	Н	m.	121	F4	PCT-US93-1	8, Applicati	ca
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53	<b>a</b> ()	51.2	-1	Ç,	-22-08-81	r.	CI
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16	489	-4	<b>+1</b>	w	-224-80-SD	104, Applica	2.170-3
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18	489	ij	17.	9	US-08-477-	72, Applicat	2.17e-3
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                                                                                                                                                                                                                                                                                                                                                                          METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION. VACCINATION WITH A B-CELL SUPERANTICEN AND CONJUG
                                                                                                                                                                  61 YAQNYAQKFRDRVSIIADESTSISFIELSNLRSDDTAVYYCARDPPRYCSAGRCYPG·F· 118
                                                                                                                                                        59 -T-NYAQKFQGRVTITADTSTSTAYMELSSLRSEDIAVYYCARAPG-YGSGGCYRGDYX 115
                                                                                                               1 QVQLV-QSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMG-WINPYGNGD 58
                                                                                                                                 1 EVQLLEQSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIFIFGSAN 60
                                                                                           7; Gaps
                                                                       Length 129;
                                                                                            22; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PAtentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                      Score 607, DB 13;
Pred. No. 2.43e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US93/10555 FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: FD-2630
                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application PC/TUS9310555
                                                                                                                                                                                                                                                                                                                         Sequence 13, Application PC/TUS9310555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                        MOLECULE TYPE: protein
JENCE 129 AA; 13930 MW; 96169 CN;
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SILVERMAN, GREGG J. TITLE OF INVENTION: METHOD FOR ITLE OF INVENTION: VARIABLE R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13:
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51
                                                                                                                                                                                                                                                               STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 amino acids
 LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                      63.5%;
ilarity 67.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF INVENTION: THI
NUMBER OF SEQUENCES: 5:
COPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90067
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Los Angeles
California
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                                                                                                                                                                                                             119 FQQWGQGTLVTVSS 132
                                linear
                                                                                                                                                                                                 116 FDYWGQGTLVTVSS 129
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90067
                                                                                  Local Similarity
les 90; Conser
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                                 TOPOLOGY:
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                                                     SECUENCE
                                                                         Query Match
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METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIHODIES
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                                                                                                                                                                                                                                                                                                                           62 AQNYAQKFADRVSIIADESTSTSFIELSNLRSDDIAVYCARDPPPYCSACHCYPGFFQO 121
                                                                                                                                                                                                                                                                                                          57 A-NYAQKFQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKFG--YGDYGRPF-DF--- 109
                                                                                                                                                                                                                                                  2 VOLLEGSSARVEKPGSSVKVSCKASGGFFSGHVITWVPQAPGGGFFWGFSIPIFGSANY 51
                                                                                                                                                                                                                          1 VHLV-QSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFG--U- 56
                                                                                                                                    Score 559, DR 11: Length 120;
Pred. No. 2.79e-37,
16: Mismatches 14; Indels 11; Gaps
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APPLICATION NUMBER: PCT/US93/10~7
FILING DATE: 29-0~~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS. St.
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application PC/TUS9310555.
                                                         NAME/KEY: Peptide
LOCATION: 1..120
NCE 120 AA; 13008 MW; 78865 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SILVERMAN, GREGG J. TITLE OF INVENTION: METHOD FOR TITLE OF INVENTION: VARIABLE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER FD TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1
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COMPUTER READABLE FORM:
                                                                                                                                        Query Match
Best Local Similarity 68.7%,
Matches 90, Conservative
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STATE: California
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IMMEDIATE SOUPCE.
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PCT-US93-10555-12
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                 CLONE:
FEATURE:
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                                                                                                       SEQUENCE
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                                                                                                                                                       20; Mismatches 13; Indels 11; Gaps
                                                                                                       1 VQLV-QSGAEVKKPGSSVKVTCKASGDTFSSSAISWVRQAPGQGLEWMGGIIPIFGTPNY 59
                                                                                                                         2 VQLLEQSGAEVPKPGSSVKVSCKASGGIFSGHVIIWVRQAPGGGLEWMGESIPIFGSANY 61
                                                                 Score 539; DR 11; Length 120;
Pred No. 1 36e-35;
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Prod No 9 446-25;
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APPLICATION NUMBER: 115/08/217 919
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION -
APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LARS
APPLICANT: OSTBERG, LARS
ITLE OF INVENTION: HOMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
                                                                                                                                                                                                                                         147 AA
                                                                                                                                                                                                                                         PPT.
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JENCE 147 AA; 15801 MW; 123306 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PG compatible OPERATING SYSTEM: PG-EGS/MS-DGS
                           NAME/KET: Peptide
LOCALION: 1.120
KCE 120 AA: 12984 MW: 80846 CN;
                                                                                                                                                                                                                                                                                                                 Sequence 4. Application US/NR217918
Patent No. 5506132
                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08217918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24-MAR-1994
CLASIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: Smith, Willaim M
REGIETPATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEBRONE: (415) 336-2400
TELEBRAX: (415) 326-2422
INFORMATION FOR SEC. 11 No. 4.
SEQUENCE CHAPACTEDISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                           STREET 379 Lytton Avenue CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 38.
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
                                                                 Query Match
Best Local Similarity 66.4%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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 IMMEDIATE SUURCE:
                                                                                                                                                                                110 WGQGTLVTVSS 120
                                                                                                                                                                                                   122 WGQGTLVTVSS 132
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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           CLONE
                    FEATURE
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                                                SECUENCE
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78 -T--YAQKFQGRVTISADASTSTAYMELSSLRSDDTAMYYCARDITA-PGAAPTPLNFYG 133
                                                                                  1 EVOLLEGGSGAEVRKPGSSVKVSCKASGGTFSGHVIIWVPGAPGGGGLEWMGESIPLEGSAN 60
                                           20 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSNFATSWVFQAPGQGLEWMGRIMPLFVTS- 77
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9; Gaps
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APPLICANT: Lonberg, Nils
APPLICANT: Ray, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Watch
Local Similarity 74.8%; Prod. No. 1.42e-33;
Hes 77; Conservative 13; Mismatches 8: Indele
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ADDRESSEE: William M. Smith
STPEET: One Market Plaza, Steuart Tower, Suite 2000
86: Conservative 20: Mismatches 20: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PCTODS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.25
CUPRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06185
FILING DATE: 19910828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 -A-NYAOKPOGRVIITADKSISTAYMELSSLRSEDTAVYYCAR 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
JENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEFEPENCE/DOCKET NIMBER- 14.
TELECOMMUNICATION INPOFMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFOPMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 87654
                                                                                                                                                                                                                                                                                                                                                    STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDAGEST: ONG MAINE COLIY: San Francisco
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MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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PCT-8592-06185-55
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13; Mismatches
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                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: peptide
JENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 63, Application US/U8U53131
Patent No. 5661016
GENERAL INFORMATION:
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                                                                                                                                                                     F: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                     30,223
                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,2
                                                                                                                                                                                                                                                                                                                                                                   102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                oue Market Pl
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                        single
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CORRESPONDENCE ADDRESS:
                                                                 NUMBER OF SEQUENCES: 7
                                                                                                                                                          COMPUTER PEADABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 74.8%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              San Francisco
                                                                                                                                                                                                                                                                                                                                                                              AMINO ACID
Patent No. 5633425
GENERAL INFORMATION:
                                                                                                                                                                                                                                                   CLASSIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                               94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 515; DB 10; Length 192;
Pred. No. 1.42e-33;
13; Mismatches 8; Indels 5; Gaps
                                                                                                                                                               APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
CORPRESPONDENCES: 152
                                                                                                                                                                                                                                  7: William M. Smith
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 -A-NYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YAONYAOKERDRVSIIADESTSTSFIELSNLRSDDTAVYCAR 103
  61 YAQNYAQKFRDRVSIIADESTSTSFIELSNI,RSDDTAVYYCAR 103
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                                                102 AA
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                                                                                                                                                                                                                                                                                                                                                                     PCT/US92/10983
                                                PRT;
                                                                                                                                       63, Application PC/TUS9210983 INFORMATION:
                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 55, Application US/07834539A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/07834539A.
                                                                                                                   Sequence 63, Application PC/TUS9210983
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM - MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 14(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                            30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-326-2422
INFORMATION FOR SPO ID NO: 63.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD,
                                                 STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Smith, William M. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                               19921217
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Aatches 77, Conservative
                                                                                                                                                                                                                                                        San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-834-539A-55
                                                 PCT-US92-10983-63
                                                                                                                                                                                                                                                                                         94105
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                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                          Sequence 63,
GENERAL INFO
                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                    STATE:
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                                                                                                01-JAN-1900
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APPLICANT: Lonberg, Nils
APPLICANT: Kay, RObert M.
TITLE OF INVENTION: Producing Heterologous Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5651015-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodhes
NUMBER OF SEQUENCES: 197
                                                                                                                                                                        E: William M. Smith
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E_{\rm c} Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.9%; Score 515; DB 7: Lenath 102; 74.8%; Pred. No. 1.42e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/67/834,539A
FILING DATE: 19920205
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLLEÇSGAEVEKPGSSVKVSCKASGGTESGHVITWVPQAPGGGLEWMGESIPIFSSAN 60
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GENERAL INFORMATION.
APPLICAT. THE SCIPES RESEARCH INSTITUTE
TILLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPPER
TILLE OF INVENTION: SIMPLEX VIPUS AND METHODS THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match Similarity 74 9%, Score 515: DR 7: Length 102; Local Similarity 74 9%, Prod No. 1 426-33. Asservative 13: Mismatches 8, Indels
                                             MEDIUM TYPE: FLAPPY disk
COMPUTER: IBM PC COMPATIBLE
OFBRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pc-DoS/MS-DOS
SOFTWARE: Patentin Pc-DoS/MS-DOS
SOFTWARE: Patentin Pc-DoS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FLING DATE: 15-APP 1993
CLASSIFICATION NUMBER: US 07/990,860
FILING DATE: 16-DC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/853,408
FILING DATE: 11-DEC-1991
PRIOR APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTONESYAGENT INPOMENTION:
NAME: SMITH: WAILLIAM MARE:
PFGISTPATION NUMBER: 30, 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 -A-NYAOKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YAQNYAQKERDEVSIIADESTSTSFIELSNERSDDTAVYYCAR 103
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STREET: 1880 Century Park East, Stite Ego
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                       14643-9-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE, protein
JENCE 102 AA: 10940 MW: 55781 CN:
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                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                     : 102 amino acids
amino acid
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                                    COMPUTER READABLE FORM MEDIUM TYPE: Floppy
California
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            COUNTRY:
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STATE:
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60 ---KFQDPLTITADVSTSTAYMQLSGLTYEDTAMYYCAP-VA-YMLEPTVTAGGLDVWGQ 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 LEGSGAEVPKPGSSVKVSCKASGGTFSCHVITWVRQAPQGGLEWMGESIPIFGSANYAQN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6: Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application PC/TUS9311612
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
TITLE OF INVENTION: L.Selectin
NUMBER OF SEQUENCES: 12
CORRESPONDER ANDRESS:
ADDRESSE: Townsend and Townsend Khourie and Grew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 515: DB 13: Length 122: Pred. No. 1.42e-33: 20: Mismatches 21: Indels
COMPUTER: 1BM PC compatible
OPERATIVE SYSTEM: PC-10/8/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUPRINT APPLICATION NATA:
APPLICATION NUMBER: PCT/US45/N0067
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COMPUTER: IRM PC compatible
OPERATING SYSTEM: DC-0.5/AS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                JMBER PCT/US95/00067
Q4-JAN-1995
                                                                                                                                                                                                                      FD-3229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide
LOCATION 1, 122
VIE 122 AA; 12999 WW; R6612 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application PC/TUS9311612.
                                                                                                                                                                                                               PEFBENCELONGER UNMARER - FD-3;
PELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDAMD:
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CLONE: FabHSV 8
                                                                                                          FILING DATE: 04
CLASSIFICATION:
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PCT-US93-11612-8
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US-08-844-215-1.rai

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SEQUENCE
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57 -GTKYNEKFKGRVTITSDESTNTAYMELSSLRSEDTAVYYCAREE--Y---GN-YVRYFV 109
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                                                                                                                                                                                                                                  1 QVQLV-QSGAEVKKPGSSVKVSCKASGYTFTSYVMHWVRQAPGQGLEWIG--Y-IYPYND 56
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Pred. No. 2.54e-33;
24; Mismatches 16; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application PC/TUS9311612
GENDRAL INFORMATION:
APPLICANT: CO, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 12
COPRESSONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER TRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                               140 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IS 07/983.946
FILING DATE: 01-DEC-1992
 APPLICATION NUMBER - PCT/US93/11612
                                                                                                                                                                                                                                                                                                                                                                PRT:
                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
                                                                                11823-22
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application PC/TUS9311612
                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 121 AA; 13661 MW; 87993 CN;
                                                                             REFERENCE/DOCKET NUMBER. 115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                         30,223
                                                                                                       TELFERA 415-326-2422
INFORMATION FOR SEV ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                STANDARD
                                                                                                                                    LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                  Match 53.68;
Local Similarity 61.48;
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California
                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                linear
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                     CLASSIFICATION:
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PCT-US93-11612-12
            FILING DATE
                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1900
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                      Matches
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76 -GTKYNEKFKGRVIITSDESTNTAYMELSSLRSEDTAVYYCAREE--Y---GN-YVKYFD 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLV-OSGAEVKKFGSSVKVSCKASGYTFTSYVMHWVRQAPGGGLEWIG--Y-IYHYND 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Mismatches 16; Indels 11;
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Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: GUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HIMMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 512; DB 11; Length 140:
Pred. No. 2.54e-33;
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PRIOR APPLICATION DATE: 07 ASSETS
APPLICATION NUMBER: 05 ASSETS
FILING DATE: 15 ASSETS
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                                                                                                                        11823-22
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SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
JENCE 140 AA, 15650 MW; 117746 CN;
                                                                                                           REFERENCE/DOCKET NUMBER: 1182.
TELECOMMUNICATION INFOPMATION:
TELEFAX, 415-326-2400
TELEFAX, 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
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                                                                                    30,223
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PRIOR APPLICATION DATA:
AFFLICATION NUMBER: US 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995
N: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              : 140 amino acids
amino acid
                                   NAME: Smith, William M. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Local Similarity 61.4%;
nes 81; Conservative
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FILING DATE: 07-JUN
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California
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1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSFSATTWVPQAPGQGLEWMGGIVPMFGPPN 59
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Patent No. 558508
GENERAL INFORMATION:
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SLICK, Harold E.
IIILE OF INVENTION: IMPROVED HIMANIZED IMMINISTIONS
NUMBER OF SEQUENCES: 113
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Pred. No. 2.17e-31;
16, Mismatches 9, Indels
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COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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      PRIOR-APPLICATION DATA

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28,9EC.1989

ATTORNEY AGENT INFORMATION

NAME: Smith, William M

PECISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002600

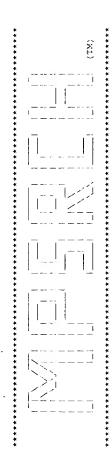
TELEFONMUNICATION INFORMATION:
TELEPHONE: (415,326-2400

TELEPANE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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FILING DATE: 13-FER-1989
                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO FEATURE
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Best Local Similarity 70.6%;
Matches 72, Conservative
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COMPUTER READABLE FORM:
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CLASSIFICATION: 424
PRICE APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                            TYPE:
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1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSRSAJIWVPQAPGQGGFFWMGGTVPMFGPPN 59
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OTHER INFORMATION: /note≈ "Eu heavy chain amino acid
OTHER INFORMATION: sequence"
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TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
TUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
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Pred. No. 2.17e-31;
16, Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 YAQ----KFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA 97
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 11823-002500 TELECOMMUNICATION INFORMATION
                                                     APPLICATION NUMBER 1990
FILING DATE: 28-SEP-1990
RION APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENI INFORMATION:
NAME: Smith, William M
PEGISPRATION NUMBER: 30,223
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US 07/634,278
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APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
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TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 15-
SEQUENCE CHARACTERISTICS:
                      19-DEC-1990
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
APPLICATION NUMBER: 19-DEC-1
FILING DATE: 19-DEC-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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Best Local Similarity 70.6%;
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STFANDEDNESS: si
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Job time : 16 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
LOCATION: 1.117
LOCATION: 1.117
OTHER INFORMATION: Anote-"Eu heavy chain amino acid
OTHER INFORMATION: sequence."
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APPLICANT: QUEEN, Sunq
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: CARDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELLCK, Aarold E.
APPLICANT: SELLCK, Aarold E.
NITIE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 489; DB 6; Length 117;
Pred. No. 2.17e-31;
16; Mismatches 9, Indels
                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YAQ----KFQGRVTITADESTNTAYMELSSLRSEDIAFYFCA 97
                                                                                                                                                                                                                                                           11823-002600
                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
                                                                   JMBER: US/07/634,278
                                                                                                                                                                                              US 07/290,975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION sequence."
117 AA: 12472 MW: 77871 CN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 72, Application US/07634278.
                                                                                                                                                                  FILING DATE: 13-FEB-198
PRIOR APPLICATION DATA:
APPLICATION NUMBRR: US 07/290
FILING DATE: 28-DEC-1988
ATTOPNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET UNMRER: 1182:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-2400
TELEFAX. (415) 326-2422
INFORMATION FOR SEQ ID NO. 15:
SEQUENCE CHARACTERISTICS:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                 117 amino acids
                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                       : protein
                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.2%;
Best Local Similarity 70.6%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                      unknown
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APPLICANT: QUEEN,
                                                                                     FILING DATE: 19
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-634-278-72
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSFRATTWVKQAPGGGLEWMGGTVPMFGPFN 59
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70.6%; Pred. No. 2.17c-31;
Ative 16; Mismatches 9; Indels 5; Gaps
CORRESPONDENCE ADDRESS: AppRESSEE: Townsend Khourie and Crew
                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28 SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
                                                                                                                                                                                                                                                               US/07/634,278
                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: peptide
JENCE 117 AA; 12472 MW; 77871 CN;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30,223
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INFORMATION FOR SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 326-2400
                                        379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Smith, William M
                                                                                                                                                                                                                                                                                19-DEC-1990
                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 amino acids
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Matches 72; Conservative
                                                                                                                                         COMPUTER READARLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER
                                                                                                                                                                                                                                                               APPLICATION NUMBER:
FILING DATE: 19-DEC
                                                                Palo Alto
California
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Pelease 2 1D John F Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, H K Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07.02.25 1998. Master time 8.25 Seconds 487.247 Million cell updates/sec Run cr.

Tabular output not generated

>US-08-844-215-1 (1-132) from US08944215.pep 956 1 EVQLLEQSGAEVPKPGSSVK... Title: Description: Perfect Score:

Sequence:

PCYPGFFQQWGQGTLVTVSS 132

PAM 150 Gap 11 Scoring table:

95051 segs, 30469580 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing.

Database:

liannl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann9 13:unann9 14:unann10 15:unann11 16:unann12 17:unenc

Mean 41.620; Variance 105.958: scale 0 393 Statistics: Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length	P.C.	I.D	Description	Pred. No.
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C1	584	-4	CI 더	۲.	100	Id heavy chain V red	C 3
m	579	ب ب ب	129	7	A33548	heavy chain V-	7.540-71
4	577	0	127	7	10	Iq heavy chain V req	.57e-7
Ω	575	60 1	725	7	B33548	heavy chain V-	3 270-70
9	567	6.00	160	^	c.	Ψ.	100-5
7	566	σh	001	^	FH0952	7.	.80e-6
œ	260	ά	135	٢	PH0953	q heavy chain V	7.90e-58
0	559	58.5	132	۲.	PH0954	d hearry chain V	1.14e-67
10	551	57.6	129	۲.	836260	Id heavy chain V red	2.11e-66
11	549	7	116	1	S36261	heavy chain V	
13	546	7	121	7	A49590	heavy chain v	1.31e-65
13	546	57 1	132	۲.	246394	heavy chain V	1.310-65
14	545	57.0	133	7	C33548	heavy chain V-	.89e-6
15	545	~	627	_	S14683	Ig mu chain precurso	1 896-65
16	544	9	126	1	DHOOKU	heavy cha	2.726-55
17	542	500	116	۲.	PHOPES	chain V	59-045-52
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61	538	56.3	577	7	PHO961		2 420-64
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113 diwaggtivtvss 125 : |-|||||||||||||||||| 123 @@WG@GIIVIVSS 132

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3.49e-64 2.49e-64	4.99-6	.236-6	. 25e-b	10e-6	330-6	.51e-6	.04e-6	040-6	15e-5	.4le-6	93e-5	110-5	ď.	.11e.5	.98e-5	.29e-5	.660-5	10 10 10 10 10 10 10 10 10 10 10 10 10 1	.13e-5	326-5	2E - 5	.02e-5	.90e-5
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PH0957  #type fragment	eren	le es	#region framework l\ #domain immunoglobulin homology #label IMM\ #region complementarity-determining l\ #region complementarity-determining 2\ #region complementarity-determining 2\ #region complementarity-determining 3\ #region complementarity-determining 3 #length 125 #checksum 8143	56.1%; Score 632; DB 7; Length 125; Similarity 72.9%; Pred. No. 2.62e-79; 97; Conservative 15, Mismatches 12; Indels 9; Gap	<pre>qvqlv-qsgacvkkpgssvkvsckasgatissyainwvrqapgqqlewmqqiipiiqtan 59 illillillillillillillillillillillillill</pre>
RESULT 1 ENTRY TITLE OPGANISM DATE ACCESSIONS REFERENCE	#authors #journal #title #cross.ref #accession	##status ##molecule ##residues CLASSIFICATION KEYWORDS FFATURE	1-30 15-98 31-35 36-50 51-67 68-98 29-113	Doory Ma Post Loc Matches	27 1 8 19 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9

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#title Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
                                                                                                                                                                                                                                                                                                                                                *superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of matural autoantibedies.
**Teross-references MUID:92202880
                                                                                                                                                                  #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MyID:92202880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapgqglewmggiipifgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVOLLEOSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIPIFGSAN 60
                    PH0952 #type fragment
Ig heavy chain V region (66+ CLL-SMI) - human (fragment)
#formal_name Homo sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Gaps
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#formal_name Homo sapiens #common_name man
17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin homology #label IMM\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 128;
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Pred. No. 1.21e-71;
18; Mismatches 17; Indels
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Best Local Similarity 67.9%;
Matches 91; Conservative
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                                                                                                        16-Aug-1996
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                                            TITLE
ORGANISM
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68-98
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1-129 **label MAR *superfamily immunoglobulin homology
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#journal Exp Med (1992) 175:988-991

#title Evidence for somatic selection of natural autoantibodies.

#cocss.references MID:92202880

#accession PH0955
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                                                                                                                                                                                      immunoglobulin homelegy #label IMM\
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 579; DB 7; Length 129;
Pred No. 7.54e-71;
16; Mismatches 19; Indels
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#region framework 2\
#region complementarity-determining 2\
#region framework 3\
#region framework 3\
#region complementarity-determining 3
#length 129 #molecular-weight 13932 #chec
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#length 127 #checksum 6297
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Pred. No. 1.57e-70;
                                                                                   heterotetramer; immunoglobulin
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Best Local Similarity 68.7%;
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Best Local Similarity 66.9%;
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PH0955
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the authors translated the codon SAC for residues 108 and 109 as Glu
The antibody is one of the cold agglutinins that preferentially bind red blood cell membrane antigens at low temperature, causing cold agglutinin disease (CAD).

IION #superfamily immunoglobulin V region; immunoglobulin homelogy autoantibody; hemagglutinin
                                                                                                                                                                       *authors Kipps, T.J., Temhave, E. Pratt, L.F., Duffy, S., Chen, P.P., Carson, D.A.

*journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917

*title Proclopmentally restricted immunoglobulin neavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.

*cross-references WUID:89345575
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J Exp Med. (1989) 169:1631-1643
Pelationship of variable region genes expressed by a human B
cell lymphoma secreting pathologic anti-Pr-2 erythrocyte
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Ig heavy chain V-1 region (AND) - human
#formal_name Homo sapiens #common_name man
17-Jan-1990  #sequence_revision 17-Jan-1990  #text_change
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31-Mar-1990 #sequence_revision_31-Mar-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                      preliminary; nucleic acid sequence not shown; not
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#superfamily immunoglobulin V region: immunoglobulin hemology
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J. Exp. Med. (1992) 175:983-991
Evidence for somatic selection of natural autoantibudies.
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                                                                                                                                                                                                                          7; Gaps
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Ig heavy chain V region (G6+ T-142) - human (fragment)
#formal_name Homo sapiens #common_name man
17-April993 #Sequence_seristion if-April963 #text_shanger
16-Aug-1996
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Pred. No. 8.80e-69;
14; Mismatches 11; Indels 12; Gaps
                   #demain immuneglebulin hemelegy #label IMM\
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                                                                                                                                                                                 Score 567; DB 7: Length 160;
Pred No. 6 10e-69,
                                                                                                                                                                                                                          24; Mismatches 16; Indels
                                         #region complementarity-determining 1% #region complementarity-determining 2%
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#length 120 #checksum 5559
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#domain 14 segment #label 7sc
#domain C region #label 7sc
#length 160 #checksum 3900
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Local Similarity 64 48,
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Best Local Similarity 72.0%;
Matches 95; Conservative
                                                                                                                                                                                                                          85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  133 ywgggtlytyss 144
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145-160
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34-117
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*superfamily immunoglobulin V region; immunoglobulin homology
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#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
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#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
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Pred. No. 7.90e-68;
16; Mismatches 8; Indels 8; Gaps
Ig heavy chain V region (G6+ CLL-SIC) - human (fragment)
#formal_name Homo sapiens #cummou_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
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#length 132 #checksum 9232
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#region framework 3\
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#length 135 #checksum 2318
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66.4%; Pred. No. 1.14e-67;
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Best Local Similarity 66 4%:
watches 91; Conservative
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Griffiths, A.D.: Malmqvist, M.: Marks, J.D.: Byo, J.M.:
Embleton, M.J.: McCafferty, J.: Rajer, M.: Holliger, K.P.:
Gorick, B.D., Hughes-Jones, N.C.: Hoogenboom, H.R.: Winter.
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Embleton, M.J.: McCafferty, J.: Baier, M.: Holliqer, K.P.:
Gorick, B.D.: Hughes-Jones, N.C.: Hoogenboom, H.R.: Winter,
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Human anti-self antibodies with high specificity from phage
display libraries.
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Human anti-self antibodies with high specificity from phage
display libraries.
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                                                                         61 YAQNYAQKFRDRVSIIADESTSTSFIELSNLRSDDTAVYYCARDPPRYCSA-GRCYPGFF 119
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03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
1 EVOLLEQSGAEVRKPOSSVKVSCKASGGTFSGHVITWVRQAPGOGLEWMGESIPIFGSAN 60
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Ig heavy chain V region (clone alpha-CEA4-RA) - human
(fragment)
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Ig heavy chain V region (clone alpha-TNF-E7) · human
(fragment)
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Pred. No. 2.11e-66;
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Best Local Similarity 61.9%;
Matches 83; Conservative
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                 ##cresidues 1-116 ##label GRI
##cross-references EMBL218841
#FICALION *superfamily immunoglobulin V region: immunoglobulin homology
DS
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Ighteavy chain V region (ACHSVI, clone 15) - human (fragment)
#formal_game Home appleas #formal_game man
06-oct-1994 #sequence_revision 18-Nov-1994 #text_change
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##molecule_type nucleic acid
##residues 1-121 ##label BUP
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Igheavy chain V region - human
#formal_name Homo sapiens #common_name man
27.Jan-1995 #sequence_revision 27.Jan-1995 #text_change
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#title Recombinant human Fab to glycoprotein D neutralizes
infectivity and prevents cell to-cell transmission
hcross-references MUID:94105168
                                                                                                                         #domain immunoglobulin homology #label IMM
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Matches 81; Conservative
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Pred No. 1.31e-65;
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##experimental_source bone marrow lymphocytes
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Best Local Similarity 64.3%;
Matches 81; Conservative
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##molecule_type mRNA
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#Litle Proc. Natl. Acad. Sci U.S.A. (1989) 86:5913-5917
#Litle Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
#cross.references MUID:89345575
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FICALION #superfamily immortable V region; immortagion homology
DS heterotetramer; immunoglobulin
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545390
Figini, M.; Marks, J.D.; Winter, G.: Griffiths, A.D.
J. Mol. Riol. (1994) 239:68-78
In Vitro assembly of repertoires of antibody chains on the
surface of phage by renaturation.
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Pred No 1.31e-65;
20; Mismatches 18; Indels 10; Gaps
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Ig heavy chain v-1 region (783) - human
Ig heavy schain v-2 sapiens #common_name man
17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
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compared with conceptual translation
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Best Local Similarity 65.0%:
Matches 89; Conservative
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##residues 1-627 ##label FRI ##residues ##cross-references EMBL:X17115 CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology KEYWORDS immunoglobulin; membrane protein
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#product Ig mu chain #status predicted #label MAT\
#domain immunoglobulin homology #label IMM
#length 627 #molecular-Weight 68510 #checksum 8581
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Ig mu chain precursor, membrane-bound (clone 201) - human
#formal_name Homo sapiens #common_name man
31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
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57.0%; Score 545; DB 7; Length 627;
Best Local Similarity 66.4%; Pred. No. 1.89e-65;
Matches 93; Conservative 20; Mismatches 12; Indels 15; Gaps
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114 dyyyygmdvwgggttvtvss 133
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118 ---FF-QO-WGGGTLVTVSS 132
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S14683; S08047
                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                 S14683
                                                                                                                                                                                                    ACCESSIONS
REFERENCE
#authors
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16-627
34-117
                                                                                                                                  TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARY
                                                                                             RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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MPsrch_pp prot	protein - protein database search, using Smith-Waterman algorithm
Run on:	Tue Feb 24 07:01:43 1998; MasPar time 5.55 Seconds
Tabular output n	504.423 Million CHII Updates/Sec not generated.
Title: Description: Perfect Score: Sequence:	>US-08-844-215-1 (1-132) from US08844215.pep 956 : EVQLLEQSGAEVPKPGSSVK PCYPRFPQQWQQGTLVIVSS 132
Scoring table:	РАМ 150 Gap 11
Searched:	59021 seqs, 21210388 residues
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database.	<pre>swiss-prot34 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7 part7 8:part8 9:part9 10:part10 11:part11</pre>
Statistics:	Mean 42 359; Variance 75 508; scale 0.561
Pred. No. Score grea and is der	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, i derived by analysis of the total score distribution.
	SUMMARIES

	Pred No.	1 226.81	7 540-72	9 650-71	7 190-58	3 300-67	1 900-65	1.44e-64	3,000-63	4.970-53	4.976.63	1.27e-60	1.270-60	1.940-58	3 210-58	3.946-57	6.508-57	6 506-57	7 940-56	5.86e-55	5.86e-55	9.566-55	2,620-54
SUMMARIES	ption	VY CHAIN V-I FE	VY CHAIN PPECTIF	CHAIN	CHAIN	CHAIN P	VY CHAIN PPECUP	VY CHAIN V REGI	VY CHAIN V-I RE	VY CHAIN V-I PE	VY CHAIN V-III	VY CHAIN V REGI	VY CHAIN V-III	VY CHAIN PRECUR	VY CHAIN V-I FE	VY CHAIN V REGI	VY CHAIN PPECUP	CHAIN	VY CHAIN PPFCUP	VY CHAIN PRECUR	VY CHAIN V REGI	OY CHAIN PPECUR	CHAIN
	Description			N IG HEAVY				•	, .				S	E IG HEAVY			E IG HEAVY					E IG HEAVY	,
	ID	HV1A_HUMAN	HV1B_HUMAN	HV1G HUMAI	HV00_MOUSE	HV1C_HUMA	HV02_MOUSE	HV03_MOUSE	HV1E_HUMAN	HV1F_HUMAN	HV3K_HUMAN	HV01_MOUSE	HV3G_HUMAN	HV05_MOUSE	HV1D_HUMAN	HV13_MOUSE	HV04_MOUSE	HV12_MOUSE	HV52_MOUSE	HV14_MOUSE	HV51_MOUSE	HVOE_MOUSE	HV07_MOUSI
	DB	u i	Ŋ	ur.	ď	Ŋ	r.	m	u)	<b>L</b> O	Ľ	S	υì	นา	r.	S	S	S	Ŋ	Ŋ	വ	υ'n	u i
	Query Match Length	111	117	117	114	143	140	120	124	125	126	121	CI	r. ∈1 ∈1	124	117	117	117	117	117	118	117	33
œ	Query Match	51.2	46.5	46.0	44.7	44.4	43.5	43.1	42.5	42.4	43.4	41.2	41.2	40.2	40 1	39.5	39.4	39.4	38.9		38.5	38.4	38.2
	Score	489	445	440	427	424	416	412	406	405	405	394	394	384	383	378	377	377	372	9	368	w	365
	Result No.	1	2	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	L4 E4	C1

7.

67 DP PRI; 117 AA.

RESULT 2 ID HVIR_HUMAN STANDARD,

### 38.1 120 \$ 9.955_MOUSE IC HEAVY CHAIN V PEGIT ### 38.1 128 \$ 9.945_MOUSE IG HEAVY CHAIN PRECUR ### 45.2 37.3 122 \$ 1971_MOUSE IG HEAVY CHAIN PRECUR ### 45.3 37.4 122 \$ 1971_MOUSE IG HEAVY CHAIN PRECUR ### 45.3 12.1 12.5 1974_MOUSE IG HEAVY CHAIN PRECUR ### 45.0 11.5 1974_MOUSE IG HEAVY CHAIN VIII \$ 19.3 19.1 19.5 1974_MOUSE IG HEAVY CHAIN PRECUR ### 45.0 11.5 19.4 2.2 10.5 1974_MOUSE IG HEAVY CHAIN PRECUR ### 45.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 35.0 11.5 19.4 19.5 19.5 19.5 19.5 19.5 19.5 19.5 19.5	[1] [1] [1] [1] [1] [1] [1] [1] [1] [1]
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                                                                                                                                                                                                                                                                                                                       Gaps
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                                                       HOMO SAPIENS (HUMAN).
EUKAPYOTA: METAZOA; CHORDATA; VEPTEBRATA; TETRAPODA: MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
IG HEAVY CHAIN PRECURSON V-1 PESTON (V45).
HOMO SAPIENS (HUMAN)
EUTRAPYJA - METAZÓA: GHUPEATA; VERIERATA; TETRAPUDA MAMMALLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATSUDA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q. OHNO H., FUKUHARA S., HONJO T., EMBO J. 7:1047-1051(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
O
                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION (HG3)
                                                                                                                                                                                                                                                                                          Score 445; DB 5; Length 117;
Pred. No. 7.54e-72;
17; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION (V35)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match

46 0%. Score 440: DR 5: Length 117:
Best Local Similarity 66.0%; Pred. No. 9.65e-71;
Matches 68; Conservative 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 -stsyaqkfqgrvtmtrdtststvymelsslrsedtavyycar 117
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YAQNYAQKFRDRVSIIADESTSTSFIELSNLRSDDTAVYYCAR 103
                                                                                                        117 AA; 12946 MW; BCCBB1DB CRC32;
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20 117 IG HEAVY CHAIN V
117 117
117 AA; 13009 MW FAASSODI CPC32,
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1996 (PEL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PHECHESOP V-1 PEGION (HG3)
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                                                                                                                                                                                PIR, A02624; HVHUHG
HSSP; P01810; 1FVB.
IMMUNOGLORULIN V PEGION; SIGNAL.
                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 66.0%;
Matches 68; Conservative
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                                                                                                                                                                                                                                                    117
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                                                                                    EUTHERIA; PPIMATES
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CAPPA J C. NISCHOFF A.;
J. IMMUNOL. 123:279-284(1979).
-1. ANTIBODY ISOLATED PROM TEN MICE WAS EXCLUSIVELY OF THE 1663
SUBCLASS. THERE WAS NO HETHROSENELTY IN THE HEAVY CHAIN V REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Indels '; Caps
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KNIEN T.H., WILZAARD H.V., HOWSHION M., DEPRYSHIPE P.P., VINEY J.,
BELL L.O., SOLLD H.J.;
PROC. NATL ACAD, SCI U.S.A. 79-6661-6667(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BENNICH H.H., JOHANSSON S.G.O., VON BAHK-LINDSTROM H.;
BENNICH H.H., JOHANSSON S.G.O., VON BAHK-LINDSTROM H.;
III. IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND IDEVELOPMENTS.
PACH M K., ED., FR. 1-3 F. MARCHI, DEKKER, NEW YORY. (1978).
-!- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
-!- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
HSSP, POD1607; IFGV.
IMMEDIATIONALIZED FROM A MYELOMA PROTEIN.
IMMEDIATIONALIZED FROM A MYELOMA PROTEIN.
                                                                                                                                                                                                       EUKARYOIA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA; MAMMALIA;
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EUKARYOTA; METAZOA; CHOPPATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.7%; Score 427; DB 5; Length 114; 63.3%; Pred. No. 7.19e-68; vative 22; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 yp-nyaqkfqgrvtitadestntaymelsslrsedtavyfcavrvisry 104
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21-JJL-1996 (PEL 01, LAST SEQUENCE UPDATE)
21-JJL-1996 (PEL 01, LAST SEQUENCE UPDATE)
11-JN-V-1999 (PEL 15, LAST AND FAILON UPDATE)
1G HEAVY CHAIN PRECURSOR V-1 REGION (ND) (FFAGMENTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION
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1H -> HI (1N REF. 2).

VG -> GV (1N REF. 2).

MISSING (1N REF. 2).
                                                 21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (FEL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (PEL. 01, LAST SEQUENCE UPDATE)
11. JEUL-1986 (PEL. 01, LAST ANNOTATION UPDATE)
MIS MISCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOSLOBULIN V REGION: ANTIARSONATE ANTIRODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AA; 12555 MW; 1A027F1D CRC32;
   114 AA.
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les 69, Conservative
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   STANDARD;
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111
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HSSP; P01772; 1FGV.
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BENNICH H.H., JOHAN
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HV1C_HUMAN
HV00_MOUSE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YACHYACKEPURVSIIAN-ESISISPIELSNI PSPCIAVYYCAPUPPRYCSA-GPCYPGFF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 yi-nynekfkgkttltvdksstaymqlrsltsedsavyfear--shyyg-gs-y-df-d 129
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                                                                                                                                                                                                                                                                                                                                                    30, Mismatches 23, Indels 11, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 evgl.qqsqaelvragssvkmsckasgytftsyginwvkqrpgqqlewig.yinp.gng. 75
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                                                                                                                                                                                                 Caps
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PIP: A02028: HVMSG7
HSSP: P01289: 6FAR.
IMMUNGSLOEULIN V PEGION: ANIBARSONATE ANTIRODY: HYPPITOOMA: SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.JUL.1994 (PEL. 01, PPEATED)
21.JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21.JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
13.JUL-1986 (PEL. 01, LAST ANNOTATION UPDATE)
16.HEAVY CHAIN V RECION (36-65).
MUS MUSCULUS (MOUSE).
EURARYOTA: METAZOA: CHORDATA: VEPTERRATA: TETRAPODA: MAMMALIA;
EUHEPIA: POPENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVO2_MOUSE STANDAPD: PPT: 140 AA
P01746;
21-701-1996 (REL. 11, CREATED)
C1-071-1996 (REL. 91, LAST SEQUENCE PROATE)
C1-071-1996 (REL. 94, LAST ANNOTATION PEATE)
IGHEAVY CHAIN PRECHESOR V REGION (93G7).
MUS MUSCULOS (MOUSE).
EUTARYOTA METACOR, CHOFDATA; VEFTERFATA, TETPAPODA, MAMMALIA, EUTHERIA; POPENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION (93G7).
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                                                                                   Score 424, DR F. Length 142,
Pred. No. 3.30e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMS J., PARRITTS T H ESTESS P . SLAUGHTER C., TUCKER P
                                                                                                                                                                                            24; Mismatches 73; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 416; DB 5; I
Pred No 1.90e-65;
143 AA; 16051 MW; 6D605E13 CPC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 AA; 15514 MW; 0700D5C8 CRC32;
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Best Local Similarity 51.5%;
                                                                                              Query Match
Best Local Similarity 52.6%:
Matches 70, Consernative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68, Conservative
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SCIENCE 216-309-311(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDAPP
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140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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HV03_M0USE
P01747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-A/J:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VAĞNYAÇKEREDVSITADESTSETERISMI PSTOTAVYYCARTPREPYOSANTATATATATE 120
MEDGINE, 83331846.
SIEKEVITC M., GEFTEP M.L., PRODEUF F., FIBLET R.,
MARSHAR-POTHSTEIN A.,
EDIP J. HAWINGL II.1023-1032(1982).
FEOM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
THAT HYRPIDIZE TO THIS ONE, THE AUTHORS GONGLUDE THAT ALL OF
THESE V PRSTONS HAVE PEAFPANGED TO THE SAME J SEGMENT, JH2.
HSSP, P01789; 6FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                            1 vql-qqsgaelvraqssvkmsckasgytftsyginwvkqrpqqglewig-yinp-qng-y 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VOLLEQSGAEVPKPGSSVKVSCKASGGTFSGHVITWVPQAPGGGLEWMGESTPTFGSANY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 82046599.
ANDRONS D.W., CAPRA J.D.;
BICCHEMISTRY 20:5822-5830(1981).
- I THIS CHRIN WAS ISOLATED FROM AN IGM WITH ANTI-SAMMA GLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKAPYOTA, MELAZOA: CHOPDATA: VFFTERPATA; TETRAPODA: MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                         Score 412, DB 5: Length 120:
Pred. No. 1.44e-64;
32; Mismatches 22; Indels
                                                                                                                                                                                                                           IMMUNOGLOBULIN V PEGION; ANTIAPSONATE ANTIBODY; HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fritz 124
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80
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Pred No 3 008-63;
                                                                                                                                                                                                                                                        120 120
120 AA, 33307 MW, BRARGGAL GRG32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-771-1986 (PEL 01, LAST SEQUENCE UPDATE)
21-701-1986 (PEL 01, LAST ANNOTATION UPDATE)
19 HEAVY CHAIN V-1 REGION (SIE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AA; 13732 MW; ClE9663D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUIE_HUMAN STANDAPP; P
P01761:
21-JUL-1986 (PET. 01, CPEATED)
21-JUL-1986 (PET. 01, LAST SEQU
21-JUL-1986 (PET. 01, LAST ANNO
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.4%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06
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ses 67, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A02044; MIHUSI.
HSSF; F01857; 2FGW.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
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SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                               l qvqlv-qsgaevkkpgssarlsckvsgddfntydihwvrqapgrglewm--av-vhpsdd 56
                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHOPDATA: VEPTERPATA: TETRAPODA: MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG HEAVY CHAÎN V-III REGION (KOL).
HOMO SAPIENS (HUMAN).
EUKARYOTA: METRAZOA: CHOPPOATA; VEPTERPATA: TETPAPODA; MAMMALIA:
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                Score 405, DB 5, Length 125.
Pred. No. 4.97e-53;
                                                                                                                                                                                                                                                                                                          28; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYPROLIDONE CARROXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCHMIDT W.E. JUNG H.-D., PALM W., HILSCHMANN N. HOPPE-SEYLER'S Z. PHYSIOL. CHEM 364-713-747(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 81072295.

MARQUART M., DEISRHHOFER J., HUBER R., PALM W.;

T MOL RIGH. 141.359-301(1080)

PIR: A02055: G1HUKL

PDB: 2F84; 12-JUL-89,

PPB: 2162: 12-JUL-89,

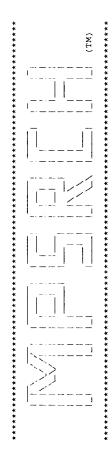
IMMUNOSIORULIN V PEGION; 30-STPUGTUPE
                                                                                                                                                                                                                                               125
13579 MW; 67450023 CRC32;
                    01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-I PEGION (MOT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P01772;
21-JUL-1986 (REL. 01, CREATED)
1-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                   V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
                                                                                                                            MEDLINE: 86203277
KOJIMA M., KOIDE I., ODANI S., ONG I.;
MOL. IMMUNOL. 23:169-174(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-PAY CPYSTALLOGPAPHY (1 9 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT:
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                                                                                                                                                                                                                                                                                             Local Similarity 47 0%;
les 62; Conservative
 STANDARD;
                                                                                                                                                                             HSSP; P01772; 8FAB.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD
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107
125
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126
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|21 QWGQGTLVTVSS 132
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                                                                                                                                                               PIR; A02025; HVHUMO.
HSSP; P01772; 8FAB.
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125
125 AA;
                                                                                           EUTHERIA: PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 83289131.
SCHMIDT W.E. JUNG
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HV1F_HUMAN
                                                                                                                                                                                                                                    DISULFID
NON_TER
SEQUENCE
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DISULMID
DISULMID
NON_TER
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DOMAIN
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                                                                                                                                                                                                                                                                             1 qvqlve-sgggvvqpgrslrlscsssgfifssyamywvrqapqkqlewv--ai-iwddus 56
                                                                                                                                                                                                                                                                                                    1 EVQLLEQSGAEVPRESSVKVS/YRAS/GTFS/GHVTTWVPQAPGQGLFWM/CESTPTFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 eagl-ggsgaelvrpgtsvkisckaagytttnywiawvkerpahalewigd---iypaaa 54
                                                                                                                                                                                                                                                     33; Mismatches 31; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA; TETRAPODA: MAMMALIA:
EUTHERIA: RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZAKUT R., COHEN J., GIVOL D.;
NUCLEIC ACIDS RES. 8-4839-4840(1980).
--- THIS SEQUENCE WAS IPANSLATED FFOM AN MPNA ISOLATED FROM A MYELOWA HAL SECRETES 1632B.
PIP: A02027: GVMS11.
HSSP; P01810; IMFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 121; Local Similarity 46.2%, Fred. No. 1.27e-60; cos 51; Conservative 38; Mismatches 22; Indels cos
                                                                                                                                                                                                                               Length 126;
                                                                                                                                                                                                                               Score 405; DB 5; 1 Pred. No. 4.97e-63;
                                                                                                                                                                                                        13718 MW; 14F328CF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 121 121
121 AA: 13135 MW: DARFORCO (1RC32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
13-AUG-1987 (REL. 05, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V FEGION (MPC 11);
                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZAKUT R., COHEN J., GIVOL D.;
NUCLEIC ACIDS RES. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                              Query Match 42.4%;
Best Local Similarity 45.9%;
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULIN V REGION.
NON_TER 121 121
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54
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108
1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS.
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STPAND
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59 y---yabsvkgritisrdbskbilylgmnslraebtanyycardrply---gb-yraf-n 110
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61 YAQNYAQKEBDRVSILALESISISPSFIFISNLPSELTAVYYYARLAPPYTSATMIYPTFFT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVOLLEGSSARVPREGSSVYVSCYASGGIFSGHVITWVFLAPGGGLEWMGESIPIFGSAN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Mismatches 29; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C5-BL/6;
MEDLINE: 81234548.
BOTHWELL A.L.M., PASKIND M., PETH M., IMANISHI-KAPI T., PAJEWSKY K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -+- THIS GERMLINE GENE RELONGS for A SEL OF CLOSELY FELATEL GENES
THAT COULD ENDORD V PESTONS OF NPR ANTIHODIES
EMBL, JODSAS, GSS4035; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEHMAN D.W., PUTNAM F.W.;
PROC. NATL. ACAD. SCI. U.S.A. 77-3239-3243(1980).
-!- THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-31-1986 (PEL 01, CPEATED)
21-31-1986 (PEL 01, LAST SPATED)
21-31-106-1986 (PEL 134, LAST SPATENCE UPDATE)
01-007-1996 (PEL 134, LAST ANNOTATION UPDATE)
1.3 HEAVY CHAIN PREPRIESOR V PETITAN (?)
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA, CHOREATA, VEPTEBRATA; IETRAFODA, MAMMALTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HONG SAFIENS (HUMAN).
EUKRANCIA, MATACCA, CHIFDAIA, VEFIEBFAIA, IETFAFCDA, MAMMALIA,
EUTHERIA: PRIMAIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYPPOLIDONE CAPPOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 394; DB 5; 1
Pred. No. 1.27e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 122
122 AA; 13668 MW; 4AF2E3D8 CPC?2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
11-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-III REGION (CAM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 41.2%;
Local Similarity 48.5%;
les 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01607; 2FGW.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD:
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CELL 24 625-637(1981).
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                                                                                             110 Swgggttltrss 121
                                                                                                                                                                                      121 OWGGGTLVTVS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A02051; M3HUAM.
HSSP: P01607; 2FGW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81013859.
                                                                                                                                                                                                                                                                                                                            LT 12
HV3G_HUMAN
F01768:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV05 MOUSE
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SEQUENCE
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Query Match 40.1%; Score 383; DB 5; Length 124;
Best Local Similarity 52.6%; Pred. No. 3.21c-58;
Matches 70; Conservative 24; Mismatches 27; Indels 12; Gaps 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
MEDLINE: 82046599.
ANDREWS D.W. CAPPA T.D.;
PITCHEMISTRY 20.5822-5827(1981).
-!-TRIS CHAIN WAS ISOLATER FROM AN ISM WITH ANTI-GAMMA GLURALIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA, CHORDATA, VEFTERFATA, TFTFAFODA, MAMMALIA;
ETTHERIA; PPIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
EUKAPYOTA, METAZOA, CHGEDATA, VERIERRATA, TETRAPOEA; MAMMALIA:
EUTHERIA; RODENTIA.
                              COMPLEMENTARITY-DETERMINING 1. PRAMEWORK 2.
                                                                                                                          COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                     40 2%; Score 384; DB 5; Length 117; 53 4%; Pred No. 1 94e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                           13016 MW; OF12FG8P CPC32;
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
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    FPAMFWOPK 1
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Bost Local Similarity 53 4%;
Watches 55; Conservative
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HSSP; P01607; 1FGV.
IMMUNOSLORULIN V PEGION
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RN [1]
RN EDLINE; 80078170.
RA SCHILLING J. CLEVINGER B., DAVIE J.M., HOOD L.;
RA SCHILLING J. CLEVINGER B., DAVIE J.M., HOOD L.;
RA SCHILLING J. CLEVINGER B., DAVIE J.M., HOOD L.;
RA SCHILLING J. CLEVINGER B., DAVIE J.M., HOOD L.;
CC 1- THE SEQUENCES OF 10 HYRPIDOMA PROTEINS THAT ALSO BIND DEXTRAN
CC THED AND J SEGMENTS.
CC 1- THIS PROTEIN RINNS DEXTPAN
DR PIRS, A26242, MHMSJ5.
DR PIRS, A26242, MHMSJ5.
DR HSSP, P01789; ZFGM.
KW IMMUNGLOBULIN V REGION.
FT NOW_TER 17 17
SO SEQUENCE 117 AA; 13024 MW; E7548A05 CRC32;
QUERY MATCH 39.5%; SCOFE 378; DB 5; Length 117;
FT NOW_TER 17 17
SO SEQUENCE 117 AA; 13024 MW; E7548A05 CRC32;
AAtches 34; Conservative 29; Mismatches 20; Indels 5; Gaps
DD 1 evql-qqsqpelvkpqasvkmckasqytftdymkwvkqshqkslewiqdinpunqqts 59
HIII - HI:: HIIII - HI:: HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HI:: URL HIIII - HIII - HIIII - HIII - HIIII - HIII ```



Release 2.10 John F. Collins, Piocomputing Pescarch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Tue Pek 24 07:05:52 1998; MasPar time 6.99 Seconds 252.448 Million cell updates/sec

not generated. Tabular output >US-08-844-215-2

EVQLLEQSGAEVKKPGSSVK.......HIMGYYFDYWGQGTLVTVSS 127 (1-127) from US08844215.pep 931 Description: Perfect Score:

PAM 150 Gap 11 Scoring table:

Sequence:

111726 segs, 13889129 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq30 Database:

i.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
B:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 15:part16 17:part17 18:part18
19:part19 20:part20 21:part12 12:part22 23:part23

Variance 161.149; scale 0.191 Mean 30.758; Statistics: Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result<br>No. | Score    | Query<br>Match | Length | DB       | ΩĪ     | Description           | Pred. No. |
|---------------|----------|----------------|--------|----------|--------|-----------------------|-----------|
| 1             | 919      | 66.2           | 147    | -1       | 855019 | 93KA9 anti-Varicella  | . 27c-3   |
| C\$           | 613      | ω,             | 123    | C3       | W19888 | EA-specific           |           |
| m             | 610      | u'i            | 487    | ı,       | -+     | غضينڪ ٻڙ ج            | α.        |
| 4             | ()<br>() | ·              | C1     |          | w1จ88จ | CEA-specific antibody | 1.650-37  |
| S             | 601      | 4.             | Ci     |          | W19886 | specific ant          | 1.986-37  |
| 9             | 009      | St             | 123    | C1       | W19881 | specific              | 2.37e-37  |
| 7             | 597      | ₹.             | CI     |          | W19887 | c anti                |           |
| ω             | 579      | ci             | C1     | œ,       | F54706 | 0:                    |           |
| σ             | 576      | 61.9           | 475    | ψ٠       | 530164 | Antibody D heavy chai | 1.90e-35  |
| 10            | 574      | Н              | 0.001  | σ        | P54795 | SpA-reactive 1gM heav |           |
| 11            | 572      | +1             | cn.    | 77       | R72068 | 늄                     | 3.94e-35  |
| 12            | 572      | 61.4           | 24     | 14       | b77610 | Humanised 501.1 VH +  | 3.946-35  |
| 13            | 565      | 0              | 12     | 14       | R75964 | HSV-neutralising anti |           |
| 14            | 561      | 60.3           | 249    |          | R77615 | Humanised 5G1.1 VH +  | 2.936-34  |
| 15            | 558      | o.             | r +    | ۲.<br>د. | W12536 | Anti-melanema antibod |           |
| 16            | 558      | 59.9           | 140    | c.       | W21847 | Humanised heavy chain | 5.06e-34  |
| 17            | 554      | 59.5           | 4      | 14       | R77616 | sed                   |           |
| 18            | 550      | 59.1           | 80.    | (1       | 872059 | HV1253 VR region.     | 2.170.33  |
| 19            | 550      | œ.             | 117    | 7        | F38623 | hearr chain           | 2.176-33  |
| C             | U)       | о.<br>О.<br>И. | 1:7    | 4        | 85.2   | Protein enfoded by th | . 17      |

| .17e-3        | 61e-3                 | .13e-3 | 13e-3         | 13          | 0e-3        | .50e-3 | .78e-3   | 3e-3     | 346-3 | .34e-3                | .33e-3 | .33e-3         | 336-3      | 336-3       | 0e - 3          | .90e-3   | 90e-3         | 27e-3                | .71e-3                | 71e-3           | .71e-3    | 71e-3    | .71e-3   | Se-3              |
|---------------|-----------------------|--------|---------------|-------------|-------------|--------|----------|----------|-------|-----------------------|--------|----------------|------------|-------------|-----------------|----------|---------------|----------------------|-----------------------|-----------------|-----------|----------|----------|-------------------|
| agment vh49.8 | Humanised heavy chain | PPG-   | Pody          | O Hymanized | artibody BI | riabl  | antibody | in vari  | rsed  | Humanised heavy chain |        | ised CDR-graft | ed 561.1 V | SAB humanis | ed humanised he | afted L2 | ed antibody L | CY1748PHB VH region. | Monoclonal antibody G | 1748PHA VH regi | B1.3∕Huma | 48PHC VH | B1.3/Hum | hain VHIS 4       |
| IO.           | W21849                | ^      | $\subset$     | 75555       |             | R50188 |          |          |       |                       |        |                |            | $\subseteq$ | R47931          | 9        | 6.            | $\overline{}$        | Η                     | ~               | 9         | αį       | φ        | Ġ                 |
|               | <u></u>               |        | σ             | c           | 9           | 6      | C1       | Ŋ        | Ŋ     | 23                    | σ      | 14             |            | ٠.          | ထ               |          | ۲٦<br>د ۱     |                      | σ                     | 11              | ထ         | 11       | œ        | 7                 |
| -1            | 7                     | C1     | C 1           | 140         | C1          | 4      | $\vdash$ | $\vdash$ | (1    | 4                     | 4      | 4              | 4          | ď           | CA              | 140      | 77            | α,                   | C 1                   | ۴.              | 3         | ۲,       | 139      | -1                |
| o,            | сh                    | ٠<br>س | α.            | σ<br>α<br>ι | ω.          | 8      | a)       | σ,<br>σ  | ъ     | ω.                    | 7.     | 7              | 7          | _           | 7               | 7        | 7             | Ġ                    | 9                     | Ġ               | 9         | 9        | 9        | Ġ                 |
| 550           | 549                   | 548    | α<br>*:<br>:: | 548         | 546         | 546    | 543      | 543      | 540   | 540                   | 535    | 535            | 7.7        | ج<br>5 ع    | 531             | 531      | 521           | 530                  | 525                   | 306             | 525       | 525      | 526      | n.i<br>C.i<br>n.i |
| 21            | C1<br>C1              | 53     | č             | Մ.<br>Ci    | 56          | 27     | 82       | 56       | 30    | 31                    | 32     | 33             | 3.4        | ٠.<br>د     | 36              | 37       | 38            | 36                   | 40                    | 7,              | 4.2       | 43       | 44       | ti i              |

## ALIGNMENTS

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subjunit of varicella zoster virus - used in a therapy and prophylaxis of infection.

Claim 8; Fig 4H: 39pp; English.

A human anti-varicella zoster virus monoclonal antibody was prophusing the triona method of Ostberg et al. (1983) Hybridona 2:351-350.

English triona neutralised vzv in the absence of complement. This cell line, designated cell line TC94RA9, produced an antibody designated 93RA9, chNA for the light and heavy chain variable region genes of the 93RA9 antibody where cloned using PCR. At least two heavy chain (gamma-1) and two light chain (kappa) specific clones were sequenced (see 082749 s 282750 respectively).
                                                                                                        Varicella zoster virus; VZW; anti-VZW monoclonal antibody; 93KA9; glycoprotein II subunit; vaccine.
                                                              02-0CT-1995 (first entry)
93RA9 anti-Varicella zoster virus antibody heavy chain variable.
                                                                                                                                                                                                                                                                                                               WOSOUCH 1994; U08241.
22-JUL-1994; US-208419.
28-JUL-1995; US-2098419.
24-MAR-1994; US-21918.
(SAMO) SANDOZ PHARM CORP.
LAKE P. USLDERG L;
WFI; 95-0906112/12.
N-FSDB; Q82750.
Human monoclonal antibodies specific for the glyco.frotein II
                                                                                                                                                         Key Location/Qualifiers
Protein 20..147
/label- mature light chain 50..54
Region 50..54
/label= complementarity determining region (CDR)
Region 69..85
LT 1
R65019 standard; Protein; 147 AA.
R65019;
                                                                                                                                                                                                                                                                        118..136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AA;
                                                                                                                                                                                                                                                                        Region
/label= CDR
                                                                                                                                                                                                                                                                                                          WO9504080-A
                                                                                                                                                                                                                                                         /lahel= CDR
                                                                                                                                             Synthetic.
                  RESULT
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Saps :: Query Match 66.2%; Score (16; DB 12; Length 147; Bost Local Similarity 66.7%; Prod. No. 1.27e 38; Matches E6; Conservative 19; Mismatches LU; Indols 1

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Seed B, Walz G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           psoriasis, etc
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09209293-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= N
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                                                                                                                                                                                                                                                                                                                                                                         /label= N
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                                                                                                                                             F24442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer 5. Cancer 6. Cardinal 4, Fig 2; 128pp; English.

Claim 4, Fig 2; 128pp; English.

This polypeptide sequence comprises the heavy chain variable region (VH), HBB1, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCBA)-specific antibody CB6 (see W19881). A claimed specific binding member (A) comprises an hCBA specific antibody antigen binding domain that has a dissociation of specific antibody antigen binding domain that has a dissociation constant for hCBA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 contracellular domain of hCBA and/or to cell-associated hCBA over hCBA over hCBA over hCBA or to cell-associated hCBA over hCBA over soluble hCBA. Preferred (A) include pairings of VH and VL sequences from CBA1-7 (see W19876-85), or their CDP sequences, as well as CBA6 VH and VL variants (see W1986-95) obtained by mitagenesis or chain shuffling. An example of a claimed pairing
                                                                         61 YAQKEQGRESITADDSTSTAYMEDSSTRSEDTAVYFCAR-VVIDNAIPHIMGYY-FDYWG 118
                                                          79 yaqkfqgrvtisadaststaymelsslrsddtamyycarditapgaaptplnfygmdvwg 138
1 qvqlv-qsgaevk>pgssvkvsckasggtfsnspinwlrqapqgglewmgsipsfgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Specific binding members for human carcinoembryonic antigen - bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutagenesis or chain shuffling. An example of a claimed pairing is HBB11 VH with CEA6 VL. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.88; Score 613; DB 23; Length 123; Best Local Similarity 72.48, Fred. No. 2.20e-38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                        tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenocarcinoma of the colon, lung or breast
                                                                                                                                                                                                                                07-DEC-1997 (first entry)
CEA-specific antibody CEA6 VH mutant HBBIl sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                          /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osbourn JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                     W19888 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCafferty JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-1996; GB-021295.
                                                                                                                                                                                                                                                                                                                                               31..35
                                                                                                                                                                                                                                                                                                     Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                        50..66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-1995; GB-025004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1996; GB-010824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1996; G03043.
                                                                                                                139 ggttvtvss 147
                                                                                                                                                                                                                                                                                                                    Chimeric synthetic.
                                                                                                                                             119 QGTLVTVSS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97-319779/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9720932-A1.
                                                                                                                                                                                                                                                                                                                                                           /label - CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.9
                                                                                                                                                                                                                              07-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Allen DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CAMB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer,
                                                                                                                                                                                                                    W19888;
                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note-
                                                                                                                                                                                                                                                                                                                                                 Region
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1 EVÖLLEÖSGAEVKKPRSSVKVSPOVERPTESPYTTOWLFQAFROREBWGNIIPVYNTPN 50

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61 YAQKFQGRLSITADDSTSTAYMELSSLRSEDTAVYFCARVVIPN-AIRHTMGYYFDVWGQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   attachment of simple Lex side chairs (see R2442, FT). The additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Pe receptor binding ability. They are preferably located in the CH2 region of the iq molecule. Antibodies bearing multiple sialyl-Lex determinants are useful for disrupting undestrable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as qyylviqsgaevkkppgssvkvsekasggtissyais⇔vrqapgqglewmagiipfifqtor R≀
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVOLLEGSGAEVKKPGSSVKVSCOVFGRTFSPYTIQMLPGAPGROPEWMGNIIPVYNTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The IgGL, in its mascent form, bears no sialyl-Lax side chains. The inventors designed a molecule including several such sites for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibition of cell adhesion mediated through ELAM-1 mol. binding

    used in treating chronic inflammation, rheumatoid arthritis,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Substn. to create glycan addition site"
Misc_difference 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 610; DB 5; 1
Pred. No. 3.81e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Sequence of antibody molecule 19G1. Antibody: immunoglobulin G1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                         .T
R24442 standard; Protein; 481 AA.
                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin G1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duery Match
Best Local Similarity 71.1%;
                                                                                                                                                                                                                                                                                                                                    02-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1991; H08605.
23-NOV-1990; US-618314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc_difference 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc_difference 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "see above"
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N-PSDB; Q25443.
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                                                                                                              117 tmvtvss 123
                                                                                                                                                                     121 TLVTVSS 127
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This polypeptide sequence comprises the heavy chain variable region (VH), HBB6, obtained by mutagenesis of the VH CDR3 of human cardionembryonic antigen (hCBA) specific antibody CER6 (see W198B1). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. An example of a claimed pairing is HBB6 VH with CEA6 VL (A) is used to defect cells expressing hCEA in vivor or in vitro, especially tumour cells for diagnosing cancer, eg. adenorationma of the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 yaqkfggrltitadeststaymelsslrsedtavyycagrshtyel-yy--yymdvwggg 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YAQKFQGRLSITADDSTSTAYMELSSLRSEDTAVYFGAPVVIPNAIPHTMGYYFDYWGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 qvqlv-qsgaevkkpgssvkvsckasggtfsnspinwlrqapgqglewmgslipsfgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLEQSGAEVKKPGSSVKVSCQVFGDTFSRYTIQWLRQAPGQGPEWMGNIIPVYNTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells, used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 64.7%: Score 602; DB 23; Length 123; Local Similarity 71.7%; Pred. No. 1.65e-37; les 91; Conservative 10; Mismatches 22; Indels
                                                                                                                                                                            CEA-specific antibody CEA6 VH mutant HBB6 sequence. Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                        /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                              "complementarity determining region 2" 99..112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCafferty JG, Osbourn JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-0cT-1996; GB-021295.
07-DEC-1995; GB-025004.
23-MAY-1996; GB-010824.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                             AT 4
W19889 standard, Protein, 123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Fig 2, 128pp; English.
                                                                                                                                                       07-DEC-1997 (first entry)
                                                                                                                                                                                                                                    adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                          Chimeric Homo sapiens;
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                    31..35
                                                                                                                                                                                                                                                                                                                                                                              50..66
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09-DEC-1996; G03043.
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144 gtlvtvss 151
                                     120 GILVIVSS 127
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60 yaqkfqgrltitadeststaymelsslrsedtayyycagcshnyel-yy-yymdywggg 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-8), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. Examples of claimed pairings are 706D10 VH with 706D12 or CEA6 VL. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 601; DB 23; Length 123;
Pred. No. 1.98e-37;
10; Mismatches 22; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide sequence comprises the heavy chain variable region (VH), Tobblo, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see Specific antibody antigen binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
                                                    07-DEC-1997 (first entry)
CEA-specific antibody CEA6 VH mutant T06D10 sequence.
Carcinoembryonic antigen, CEA; human; antibody; scFv;
tumout marker, lung cancer, breast cancer, colon cancer.
                                                                                                                                                                                                                                  /note= "complementarity determining region 1" Region 80..66
                                                                                                                                                                                                                                                                                       /note= "complementarity determining region 2"
Region
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                                                                                                                                                                                                                                                                                                                                                                                               09-DEC-1996; G03043.
11-CCT-1996; GB-021295.
07-DEC-1995; GB-02004.
23:MAX-1996, GB-010824.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                   Location/Qualifiers
JT 5
W19886 standard; Protein; 123 AA.
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Best Local Similarity 71.7%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCafferty JG,
                                                                                                                            adenocarcinoma; diagnosis.
                                                                                                                                                 Chimeric Homo sapiens;
                                                                                                                                                                Chimeric synthetic.
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WFI, 97-319779/29.
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/label= CDR3
                                   W19886;
07-DEC-1997
                                                                                                                                                                                                                   /label= CDR1
                                                                                                                                                                                                                                                                        /label= CDR2
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Claim 4, Fig la; 128pp; English.

This polypeptide sequence comprises the heavy chain variable region (VH) of human carcinoembryonic antigon (hCEA)-specific antibody CEA. VH (17126-32) and VL (172133-35) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see W19876-85).

A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant of hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human live hCEA and/or to cell-associated hCEA over hCEA over hCEA and/or to cell-associated hCEA over hCEA over hCEA cequences from CEA1-7, or their CDE sequences, as well as CEA6 VH and VL variants, including combinations of CEA6 VH with VL ceptons from CEA6, Tobog, Tobol, Lubil, Lubil, D. Lusto, Lucial, State of the Respectably tumour cells for diagnosing cancer, e.g. adenocarcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Specific binding members for human carcinoembryonic antigen - bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
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Pred. No. 2.37e-37;
10; Mismatches 22; Indels 4;
CEA-specific antibody CEA6 VH sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carcinoembryonic antigen; CEA; human; antibody; scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
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CEA-specific antibody CEA6 VH mutant HBAll sequence.
                                                                                                                                              /note= "complementarity determining region 1"
                                                                                                                                                                                                    'note= "complementarity determining region 2"
                                                                                                                                                                                                                                                         "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                       McCafferty JG, Osbourn JK;
                                                                                                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                        Location/Qualifiers
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Matches 91, Conservative
                                                         adenocarcinoma; diagnosis.
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07-DEC-1995; GB-025004.
23-MAY-1996; GB-010824.
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                                                                           Homo sapiens
                                                                                                                                                                                   /label= CDR2
                                                                                                                                                                                                                                       /label= CDR3
                                                                                                                             /label= CDR1
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                                                                                                                                                                                                                                                                                                                 09-DEC-1936,
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                                                                                                                                                                                                                                                                                                                                                                                                         Allen DJ,
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expressing beed, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocateinoma of the colon, lung or breast.
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                                            //note= "complementarity determining region 1"
80..66
                                                                                                     "complementarity determining region 3"
                                                                          "complementarity determining region 2"
                                                                                                                                                           23.MAY-1996, GB-010824.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                 Location/Qualifiers
                                                                                                                                                                                                                                       Claim 4; Fig 2; 128pp; English.
                                                                                                                                                                                McCafferty JG,
sapiens;
                                                                                                                                                   07-DEC-1995; GR-025004
                                                                                                                                 09-DEC-1996; G03043.
         Chimeric synthetic.
                                                                                                                                                                                        WPI; 97-319779/29.
                                                                                                                                                                                                                                                                                                                                                                                  123 AA;
Chimeric Homo
                                                                                                               W09720932-A1.
                                                                /label= CDR2
                                                                                             CDR3
                                     /label= CDR1
                                                                                                                         -JUN-1997
                                                                                                                                                                              Allen D.T,
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                            Region
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60 yaqkfqgrltitadeststaymelsslrsedtavyyca q.anscnrsyyyymdvrqqq 116
                                                                     1 qvqlv-qsgaevkkpgssvkvsckasgqtfsnspinwlrqapqqqlewmqsiipsfqtan 59
                                                                                                 1 EVELUBQSGAEVKPI SSVEVSPLOVESI IESEVI LJWI ELAFOQSPEWMORI ITVVNEPR 60
                                                                                                                                                                                                                                                                                                  18-007-1994 (first entry)
Spa-reactive IgM heavy chain clone KAS.
SpA domain D; Ig binding repeion: IgM: B-cell superantiven; SA4:
Superantigen; heavy chain variable region; VH3 restricted antibody;
VH, protein-A, KAS, B-lymphocyte, Haccine.
                                            4; Gaps
            pg 23; Tendth 124;
                                          Indels
                                          Mismatches 18;
                            Pred No 4 10e-37;
             1265 ATOMS
                                                                                                                                                                                                                                                                           R54796 standard; peptide; 120 AA.
                                          14:
            64 18:
Cuery Match

Best Local Similarity 71 /*,

91; Conservative
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(REGC ) UNIV CALIFORNIA 29-00T-1993; U10555. 30-00T-1992; US-969436.

Homo sapiens. Wog4Og818-A. 11-MAY-1994.

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(WELL ) WELLCOME FOUND LID.
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                                                                                                                                                                                                                                              60 aqkfqgrvtitadestntaymelrslrsddtamyycakegygdygr-p----fdfwgqgt 114
               A Simulation From the region gene family restricted antibodies - through B-cell super-antigen vaccination Disclosure; page 78; 130pp; Broflish.

A B-cell superantigen (349) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The SAG is used to enhance production of VH, septricted Abs. During attempts to identify sAgs, as a sequences (R54784-801) of H chains from Ig reactive with mod-SpA, and as and DNA sequences (FS4784-801). Of WH regions of SpA binders obtained from combinatorial libraries were determined. IgM protein RAS is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                               62 ACKRESELSTIACESISTAYMELSSLASECTAVYPOARVVIPNAIRHTMSYYFEYMGGST 121
                                                                                                                                                                                                      1 vhlv-gsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifggany 59
                                                                                                                                                                                                                        2 VQLLEQSGAEVKKFGSSVKVSCQVFGDTFSRYTIQWLRQAFGQGPEWMGNIIPVYNTPNY 61
                                                                                                                                                                                 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Heavy, light, chaim, antibody, D; monoclonal; peripheral; blood; lymphocyte, hepatitis A virus; HAV; sero; positive; patient; murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.
                                                                                                                                                            Match 62.2%; Score 579; DB 9; Length 120; Local Similarity 67.5%; Pred. No. 1.10e-35; es 85; Conservative 17; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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GB-015284.
GB-016594
GB-016594
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  Silverman GJ;
WPI; 94-167127/20.
                                                                                                                                          120 AA;
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/label= GDP2
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/label= CDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                            Sequence
                                                                                                                                                              Query Match
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                                                                                                                                                                                                                      Disclosure, Fig 2; 35pp; English.

The sequences given in R31023-24 represent the heavy and light chains of Antihody D respectively. Antihody D is a monoclonal antihody which was derived from peripheral blood lymphocytes from a hepatitis A virus (HAV) sero positive patient. Antihody D is closely related in nature to munifiedy B5B3. Total RNA was isolated from antihody D expressing cells and polydomylated RNA was extracted. Those polyh RNA's were used to prepare a cDNA library which was screened for human Further heavy (H) chains and two positive clones were detected. Sequence 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 ysqnfqgrvtitadkststahmeltslrsedtavyycatdryrqanfdrarvgw-fdpwg 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     All simulations of variable region gene family restricted antibodies - through B-cell super-antigen vaccination Disclosure; Page 77; 130pp; English.

B-cell superantigen (849) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The sad is used to enhance production of VH; restricted Abs. During attempts to identify sags, as sequences (R54784-801) of H chains from Ig reactive with mod-SpA, and as and DNA sequences (R54802-16, 02481-56) of VH regions of SpA binders bobtained from combinatorial libraries were determined. IgM protein BOR is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 qmqvv-qsgaevkkpgssvtvsckasggtfsnyaiswvrqapgqglewmggiiplfgtpt 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 vqlv-qsgaevkkpgssvkvtckasgdtfsssalswvrqapgeglewmgglipifgtpny 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVĄTILEĄSGARVKKPGSSVKVSCQVPGDTPSRYTIQWIPQAPGQGPEWMGNIIPVYNTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SpA-reactive igM heavy chain clone BOR.
SpA domain D; Ig binding region; IgM; B-cell superantigen; sAg; superantigen; heavy chain variable region; VH3 restricted antibody; VH; protein-A; BOR; B-lymphocyte; vaccine.
                                                                                         Prodn. of recombinant primate antibodies - useful for treating infections caused by hepatitis A, B and C, herpes, cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 576; DB 6;
Pred. No. 1.90e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n 10
R54795 standard; peptide; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.98;
67.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 67.4°,
87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-1994.
29-OCT-1993; U10555.
30-CCT-1992; US-969936.
(PEGC ) UNIV CALIFORNIA.
Crowe JS, Lewis AP;
WPI; 93-019951/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WFI; 94-167127/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 qgtlvtvss 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 OGTLVTVSS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 AA;
                                                              N-PSDB; Q35099
                                                                                                                                                                                                 arthritis etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9409818-A.
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                                          62 AĞKFÇGRLSITADDSTSTAYMELSSLRSEDTAVYFCARVVIPNAIRHTMGYYFDYWGÇGT 121
2 VOLLEVASIGABUKK PRISSUK VSPUVERIFFSBYTTIQMI PQADROGEPEWMRNTT PVYNTPNY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 qvqlv-qsgaevkkpgssvkvsckasgqtfssyaiswvrqapqqqlewmgqiipifgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLLEQSGAEVKKPGSSVKVSCQVFGDTFSRYTIQWLRQAPGGGPEWMGNIIPVYNTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                  by molecular cloning of immunoglobulin genes by PCR Disclosure; Page 68; 94pp. English.

L. and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (1931) genes showed homology to the closest germline genes, DP10 (089327) and hv1263 (089328). The DNA (089329) and corresp. amino acid (R72070) sequences of the VH region of a representative clone, Sequence 98 AA.
                                                                                                                                                                                                                                                                                                                                                          Graves' ophthalmopathy-associated monoclonal antibody - produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised 5G1.1 VH + IGHRL.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antihofammatory; antibody engineering;
humanised antibody; complementarity determining region; Ole
                                                                                                                                                                                  orbital antigen, monoclonal antibody; heavy chain, H chain, variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 572; DB 12; Length 98; Prod No 3,946-35; 11; Mismatches 9; Indels
                                                                                                                                                                        Graves ophthalmopathy associated immunoglobulin protein;
                     aqlfqgavtittdeststaymevsslrsedtalyycaregrimal.pp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 yaqkfqgrvtitadeststaymelsslrsedtavyycar 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                      22-SEF-1993; US-124469.
(NICH-) NICHOLS INST DIAGNOSTICS.
                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R77510 standard Protein: 249 AA
                                                                                                                               R72068 standard; Protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.4%;
Best Local Similarity 78 8%;
                                                                                                                                                   26-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                             Rapoport B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Conservative
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/label= mat_peptide
                                                                                                                                                                                                                                                                                            22-SEP-1994; U10756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45
                                                                                                                                                                                                                                                                                                                                   95-139383/18
                                                                115 lvtvss 120
                                                                                    122 LVTVSS 127
                                                                                                                                                             DP10 VH region.
                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q89327
                                                                                                                                                                                                                                                                                                                             Mclachlan SM,
                                                                                                                                                                                                                                                           /label= CDR2
                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                       /label= CDP1
                                                                                                                                                                                                                                                                                  30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R77610;
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                                                                                                                                        P72068
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Treating domerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis brample il. Fuge 119-122, 181pp. English - to inhibit complement induced cell lysis brample il. Fuge 119-122, 181pp. English - to make discovered from monse antibody control of the can be co-expressed with a humanised light chain (P77610), includes CPRs derived from monse anti-C5 monoclonal antibody 501.1. It can be co-expressed with a humanised light chain (P77612) in human 278 ERNA cells using encoding DNAS subcloned into vector APEX.*P (T08475). Such humanised recombinant antibodies retain the ability of MAP 501.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Progret is the heavy chain of the binan anti-herpes monoclonal autitody clone EachsVW. This anticody is capable of neutralising both herpes simplex virus (HSV) types I and II by binding an epitope present on diveoprotein D. The anticody may be used for detection (HSV) in vivo on in vitro; for passive immunotherapy (pref. prophylactically) of HSV infection (eq. qenital, oral or coular herpes), partie, as its Fab fragment and as a competitive reagent for detection neutralising anti-HSV antichodies in a sample. Anti-idiotypic antichodies raised against the mAb can be used for active immunotherapy of HSV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 yaqkfqgrvtmtadtststaymelsslrsedtavyycaryffgss-pu---wyfdvwqqq 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 qvqlv-qsgaevkkpgasvkvsckasgyifsnywiqwvrqapgqqlewmgeilpqsqste 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVÖLLEÖSSAEVKKPSSSVKVSCOVFGLTFSPYTIÖMLROAPSOCPEWMGNIIPVYNTPN 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HSV) types 1 and 2 - used for diagnosis and passive immuno-therapy of HSV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human monoclonal antibodies that neutralise Herpes simpley virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR 14; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derpes simplex virus, type 1, type 11, monocional antibody; diagnosis, neutralisation; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                      Rollins S;
                                                                                                                                                                                                                                                                                                                                                                      Thomas TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-1996 (first entry)
HSV-neutralising antibody clone FabHSVB heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burton DR, Sanna PP, Williamson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 572; PR 14;
Pred. No. 3.94e-35;
                                                                                                                                                                                                                                                                                                                                      Nye SH,
                                                                                                                                                                                                                                                                                                                               Evans MJ, Matis L, Mueller EE, Nye SH,
Rother RP, Springhorn J P, Squinto SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 72; 100pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quory Match
dest Local Similarity 68 58;
Watches 87; Conservative
                                                                                                                                                                                                                                                                02-MAY-1994; US-235208.
(ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JAN-1994; US-178201.
(SCRI ) SCRIPPS RES INST.
Burioni R, Burton DR, S
                                                                                                  118 130
                                   66...69
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WPI: 95-392923/50
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95-254909/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TLVTVSS 127
                                                                                                                                     /label= CDR-H3
                                                                  CDE:HC
/label= CDP-H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T08483
                                                                                                                                                                        W09529697-A1.
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                                                                                                                                                                                                        09-NOV-1995.
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                                      Region
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                                                                      label
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Search completed: Tue Feb 24 07:06:25 1998 Job time: 33 secs.
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                                                                                                                                           1 legsgaevkkpgssvkvsckasggsfssyainwvrgapggglewmgglmpifgttnyagk 60
                                                                                                   5 LEQSGAEVKKPGSSVKVSCQVFGDTFSRYTIQWLPQAPGQGPEWMGNIIPVYNTPNYAQK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 qvqlv-qsqaevkkpqasvkvsckasgyifsnywiqwvrqapgqglewmgeilpgsgste 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLLEQSGABVKKPGSSVKVSCQVFGDTFSRYTIGWLRQAPGQGPEWMGNIIPVYNTPN 60
                                                 1, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  component - to inhibit complement induced cell lysis
Claim 37: Pages 135-137: 181pp; English.
A DNA construct (108487) codes for a humanised CDP-grafted
light chain, designated 501.1 VL + IGHRLD (R77615), which includes
CDPs derived from mouse anti-C5 monoclonal antibody 561.1. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA can be subcloned together with DNA (108484) coding
for a humanised Fd (R77611) into vector APRX-38 (108476) for
expression of humanised antibody in human 293 EBNA cells. Such
recombinant antibodies retain the ability of MAb 561.1 to block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating glomerulonephritis with antibody against complement C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
                                                                                                                                                                                                                                                                              D.2-APR-1996 (first entry)

Humanised 5G1.1 VH + IGHRLD.

Complement C5: haemolysis: kidney: glomerulonephritis:
monoclonal antibody: antiinflammatory: antibody engineering:
humanised antibody. complementariry determining region: CLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.3%; Score 561; DB 14; Length 249; Best Local Similarity 64 94; Prod No. 2.93e-34; Matches 85; Conservative 16; Mismatches 21; Indels 93
                       Length 122;
                     Score 565; DB 14; Length 122
Pred. No. 1.41e-34;
14, Mismatches 26, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mueller EE, Nye SH, Rollins S; rn J P, Squinto SP, Thomas TC;
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1 19
                                                                                                                                                                                                                                           T 14
R77515 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Matis L, Mueller
P, Springhorn J P,
Wilkins JA;
                       60.78;
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-1994; US-236208.
(ALEX-) ALEXION PHARM INC
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         Ouery Match
Best Local Similarity 6
Best Local 32, Conserved
                                                                                                                                                                                                                                                                                                                                                                                        /label= sig_peptide
Peptide 20..
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WPI: 95-392923/50.
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Fig. 100m a cancer pathers

C A process for isolating and synthesising human monoclonal anti-tumour

antibodies has been produced. The process involves: (a) constructing at

antibodies has been produced. The process involves: (a) constructing at

the page library in a binding assay with cultured tumour calls of the

same type as the patient; (b) screening for anti-tumour antibodies in

the page library in a binding assay with cultured tumour calls of the

same type as the patient; stumour; (c) removing extraneous antibodies in

step (b) and (c); (e) assaying the specificity of cloning the phage selected in

step (b) and (c); (e) assaying the specificity of cloned phage that do not bind

continued tumour cells derived from more than one other tumour that is

to cultured tumour cells derived from more than one other tumour that is

continued tumour cells derived from more than one other tumour that is

continued tumour cells antibody fusion phage library, produced by

chain antibody from a VH antibody fusion phage library, produced by

a method as described above. The antibodies produced can be used for

diagnostic and therapeutic applications and for isolating tumour

continued the study and applications and for isolating tumour

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                                                                                                                                 28-ocT-1997 (first entry)
Anti-melanoma antibody 2-71 from VH antibody fusion phage library.
Human: monoclomal antitumour antibody: peripheral blood lymphocyte;
cancer: tumounigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodn. of human monoclonal anti-tumour antibodies - by screening a fusion phage library produced using peripheral blood lymphocytes
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I 15
W13536 standard; protein; 119 AA.
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30-JUN-1995, US-497647.
(UYYA.) UNIV YALE.
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WPI; 97-109061/10.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinkurgh, U.F. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn MasFar time 129.01 Seconds 825.290 Million cell updates/sec Tue Feb 24 13:29:24 1998; Run on.

Tabular output not generated.

>US-08-844-215-27 (1-378) from USU8844115.seq 378

Description: Perfect Score: N.A. Sequence Comp:

CTTTTGGTCACGTGTCTTCA 378 GAGACCAGTGGCACAGAAGT CTCCACGTCGACGAGCTCAC 1 CASSTACASCISCISSAGIC

TABLE default Gap 6 Scoring table.

Dhase 0: Query 0 SIL Nmatch 397246 seqs, 141010104 bases x D Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

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Mean 9.914; Variance 1.852; scale 5 354 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Pred. No               | 24 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -                                                                                                                                                                                       | ######################################                                                                                                                                                                                                                                | <ul> <li>4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4</li></ul>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                    | AY-1997<br>Glode Tescost<br>Filon<br>a;<br>Hominidae;<br>Jost, S.,<br>J.,                                                                                       |
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| Description            | EST1361 F2 Scarce CV3 EST1361 Tests tumor EST8960 Small intest EST8967 Small intest EXT8977 F1 Scarce OVA FST97425 Thymos II HO #449hO7 LY PATE THYMOS II HO EST13999 JEST18 LYMOP EST13999 JEST18 LYMOP EST13999 JEST18 LYMOP | EST59410 Lymft node. EST18648 Lung Homo sa EST91017 Synovial sar EST99118 Activated T- EST13423 Tosis tumor EST3322 Colon I Homo mr05907.x1 Soaros mou est5332 Tosis 1.000 mr05907.x1 Tosis 1.000 mr05907.x1 Tosis 1.000 mr05907.x1 Tosis 1.000 mr05907.x1 Stratagene | RESTORE TOTAL HORSE BENTAGE TO SOADS FOR ESTITION TO SETTING THE COMPANY TO STATE THE COMPANY TO SOAD TO SETTING THE COMPANY TO SOAD TO SOAD TO SETTING THE COMPANY TO SOAD TO SETTING THE COMPANY TO SOAD TO SOAD THE COMPANY TO SOAD TO SOAD THE COMPANY TO SOAD TO SOAD THE COMPANY TO SOAD TO SOAD THE COMPANY TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO SOAD TO | Human fetal brain obn<br>82766192 inCAP cells<br>5277412 S1 Scores Ova<br>5277412 S1 Scores Ova<br>7317410 S1 Stratugene<br>7317410 S1 Stratugene<br>7217410 S1 Scores Nob<br>721742 Scores pro<br>721760 S1 Knowles S1<br>721760711 Pancreas tu<br>8777711 71 Scores Tu | EST 16-M CHAIN PHECHSON V-1 P THAIN PHECHSON Chordat Primates, Catarrhini: Dubuque,T., Geisel,G. n.G., Marra,M., Martin De,M., Tan,F., Theisin                  |
| S E E                  | AA221281<br>AA37074<br>AA377128<br>AA402547<br>AA402547<br>AA40295<br>AA360195<br>AA360195                                                                                                                                     |                                                                                                                                                                                                                                                                       | ちょうり でまり ひこうりょうりょう ちょうりょう りょうりょう しょうしょう                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | HUMODIA09B<br>AA397232<br>AA4397232<br>AA423925<br>AA423925<br>AA423927<br>AA423957<br>AA439554<br>AA4395542<br>AA295542<br>AA295542<br>AA295542                                                                                                                         | ALIGNMENTS F. mFNA FG1; .omof NB ES1; IG HEAVY a: Eutheria; I L. Bowles,L., Le. N. Lenno ergy, K., Stept ergy, K., Stept ergy, K., Stept                        |
| ا م                    | ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~                                                                                                                                                                                          |                                                                                                                                                                                                                                                                       | 70.750.75117.38<br>10.0570.5570.<br>6.0500.0570                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 00000000000000000000000000000000000000                                                                                                                                                                                                                                   | Source to gh Mi<br>to gh Mi<br>mammali<br>to 379)<br>Allen, Milen,<br>Tacy, M.,<br>Cacy, M.,<br>Chellent<br>Yehellent<br>Yehellent<br>Yehellent<br>Yehellent    |
| %<br>Query<br>Match Le |                                                                                                                                                                                                                                | (O) O)                                                                                                                                                                                                                            | ທ່າທ່າທ່າທ່ານກໍນາ ປາ ທ້າທ້າຍກໍທ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | յ (r) (r) (r) (r) (r) (r) (r) (r) (r) (r)                                                                                                                                                                                                                                | A201381<br>'44402 r1<br>'similar<br>HUMAN).<br>A291381<br>1939359<br>SI.<br>'warritage<br>chebrata<br>Omo. Sapie<br>(bases<br>(bases<br>11107, L.<br>ucaba, T., |
| Score                  | - 80년년 80년 10년 4년 4년<br>- 10년년<br>-                                                                                                                                                                                            | * (1) (2) (1) (2) (3) (3) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4                                                                                                                                                                                                      | כו כו כו כו מומו נו נו נו נו מי                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ,0000000000000000000000000000000000000                                                                                                                                                                                                                                   |                                                                                                                                                                 |
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                                                                                                                                                                                                                                                                                                                                                                       modified polylinker, Site_1. Not I, Site_2. Eco RI, 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGGGGTGGGSTITITITITITITITIT 3'],
                                                                                                                                                                                                                                                                                                                                                                                                                                   double-stranded cDNA was size selected, ligated to Foo FI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vertor (Pharmacia). Library constructed by Bento Soares and M.Fatina Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <code>EST13661</code> Testis tumor Homo sapiens cDNA 5' end similar to similar to immunoglobulin mu heavy chain, VDJC regions (GB:M18512).
                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE consortium (info@imaqe.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 361.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                /note="Organ. ovary; Vector. pT7T3D (Pharmacia) with a modified polylinker, Site_1. Not I; Site_2. Eco RI, 1st
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 CTGCAGGGCTTCTGGAGGCAGCTTCAGAAGCTACAATTTCAATTGGGTGCGACAGGCCCC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 ACASAAGITTCAGGGGAGAGTCACAATTAGGGGGGAGGAATTGAGGGGGAATAAGAT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 ggttcagttggtgcagtctggacctgaggtgaagac-tgggggcc-cagtgaggtctc 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Adams.M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
                                                                                                             Louis Mo 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 72; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 ggagetgaggaacetgagatetgacgacacggecatatattaetytgega 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares ovary tumor NbHOT"
                                                             WashU-Merck EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 132; DB 99;
Pred. No 2 256.221;
                                                                                                         4444 Forest Park Parkway, Box 8501, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type-"ovarian tumor"
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                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.9%;
74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 74.5%;
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
Unpublished (1997)
                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                    COMMENT
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White, D. Sutton G. I Rizkensky F. Worlessey, F. G. Georgine, J.D., White, D. Sutton G. I Rizkensky F. Worley Walley, D. Sutton G. I Rizkensky J. Fine, L.D., Fitzgerald, E.M., Fitzhadh, W.M., Fitzhadh, J. Geodhaden, N. S., Glodek, A. Ghehm, C. L. Hanna, M. C. Hedblom, E. Hinkle, P. S. Jr., Felley, J. M., Felloy, I. C., Hanna, M. C., Hedblom, E. Hinkle, P. S. Jr., Moreno-Palanques, R.F., McDonald, L.A., Nauyen, D.T., Pelliquino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spridgs, T.A., Utterback, T.R., Weddman, J.F., L.J.Y., Bednarik, D.F., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wall, S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Pranen, P. Franch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Franch, P. Franch, M. Grober, J., Haseltine, W. A., Fields, C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For clone availability, additional sequence and expression information related to this EST, please check the Tidk Human Gene Index (http://www.t.gt.org/t.b//hdi/hdi.html)
Seg primer: MI3 Reverse.
   Garayne,J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /notu-"Organ, testis, Vector, pBJurscript SE, Site_1:
BOOR; Site_2: XhoI"
/clone_lib="Testis tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA377074 291 bp mPNA EST 21-APR-1997
EST89603 Small intestine I Homo sapiens cDNA 5' end similar to
similar to imminoglobalin heavy chain, VoJ regions (GB.214165).
AA377074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 GCTFFTAFFFTCTFFTFGAGGCTTCAGAGCTAGAATTTCAATTGGGTGCGACAGCCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AGSTGCAGCTGCTGCAGTCTGGGTCTGAGGTGAAGAGCCTGGGTCTT7GGTGAAGGTCT 6)
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Palt, C. J., Loo, N. H., Kirkboss, P. P., Woinstock, K.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medical Center (rive, Pickell)e, Mr 2085g USA
3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 119; DB 25; 1
Pred. No. 1.73e-193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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<1...>279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other_ESTS: THC166571
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81.1%;
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Best Local Similarity
Matches 154; Conserv
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ORGANISM

REFERENCE AUTHORS

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Adams M.D. Kerlavage A.R. Fleischmann. P.D. Fuldher. P.A.,
Bult, C.T. Lee, N.H. Kirkness, E.F., Weinstock, K.G. Goragne, T.D.,
Whiten, Sutton G. Blake, T.A. Brandon, P.C., Man-Wail, C.,
Clayton. P.A. Cline T.P. Cotton, M.D., Earle-Hughes, T. Fine L.D.,
Fitzgerald L.M., Fitzhugh, W.M., Eritchman, J. I., Geoghagen, N.S.,
Glodek, A. Gohn, C.E., Hanna, M.M., Fritchman, J. I., Geoghagen, N.S.,
Moreno-Palanques, P.F., McDenald, L.A., Nuyen, D.T., Pelligrino, S.M.,
Moreno-Palanques, P.F., McDenald, L.A., Nuyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Pyder, S.E., Scortt, J.L., Saudek, D.M., Shiley, P.,
Small, K.V., Spriggs, T.A., Titterback, T.P., Weidman, T.R., Li, Y.,
Bednarik, D.P., Cao, L., Copeda, M.A., Coleman, T.A., Collins, E.T.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Rozak, D.L., Kusch, C., Hungjun, J., Li, H., Melsner, P.S., Olsen, H.,
Raymond, L., Weil, Y.F., Wing, T., Xu, C., Yu, G.T., Plank, A.K.,
Fraser, M. and Venter, T.C.,
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial assessment of human gone diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MI3 Reverse.
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/clone_lib="Small intestine I"
/dcv.stage="adult"
                                                                                                                                                                                                  Homo sapiens
Eukaryotae, mitochondrial enkaryotes; Metazoa: Chordata;
Vertebrata, Mammalia: Eutheria: Primates; Catarrhin; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 aggetcagetggagtgeagtetggaggtgaggtgaagaageetqgggeeteantgaaggtet 155
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Pred. No. 3.75e-126,
0; Mismatches 34; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bioinformatics The Institute for Genomic Research The Institute for Genomic Research The Medical Center Drive, Rockville, XD 20850 USA Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 others
similar to immunoglobulin heavy chain, VDJ region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_ESTs: THC167579
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Best Local Similarit; 77.8%;
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 265)
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                                                                                                                                                                 human.
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BASE COUNT
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                                                                                                                                        Tobases 1 to 291)

Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldner, P.A.,

Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldner, P.A.,

Bult.C.J., Leen.N.H., Kirkness, E.F., Wanistock, K.G., Gocayne, J.D.,

White, O., Sutton, G. Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, P.A., Cline, T.P., Cotton, M.D., Earla-Hughes, J., Fine, L.D.,

Fliqqerald, L.M., Fitzhugh, W.M., Fritchman, T.L., Googhagen, N.S.,

Glodek, A., Gnehm, C.L., Hannan, M.C., Hadblom, E., Hinkle, P.S., Jr.,

Kelley, J.M., Kelley, J.C., Hannan, M.C., Hadblom, E., Hinkle, P.S., Jr.,

Moreno-Palanques, F.F., McDonald, L.A., Nuvyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shiley, P.,

Small, K.V., Spriggs, T.A., utterback, T.P., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kin, R.K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H.,

Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Puben, S.M.,

Dillion, P.J., Fannon, M.R., Posen, C.A., Haseltine, M.A., Fields, C.,

Fraser, C.M., and Venter, J.C.,

Initial assessment of human gene diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: arkerlav@tigr.org
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www +igr org/tdb/hgi/hgi htm!)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ small intesting, Vertor pBluescript SK., Site_1: EcoRI; Site_2: XhoI"
/clone_lib="Small intestine I"
/dev_stage="adult"
                                     -Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS AA377128 265 bp mRNA EST 21-APR-1997 DEFINITION EST89660 Small intestine I Homo sapiens cDNA 5 end similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 gigcagciggigcaalciggggcigaggigaaggagccigggicticigigaaginicg 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 tgcaaggctattggatacaccttcactgattatactatcaactgggtgcgacaggccct 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 IGCAGAGATTETRAGAGAGITERARAGETAERATTEERATTEGASTGEGACAGGCCCCT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 ggacagggaettgagtggatggatggatggatgaacceagcaaatggaggeteegaetgtgea 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Pockville, MP 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 53; Indels
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Pred. No 1.85e-176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 29 4%;
Local Similarity 75.5%;
nes 163; Conservative
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Query Match

Matches

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BASE COUNT

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FEATURES

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16-MAY-1997

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RESULT

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zu47h07.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 741181
5' similar to gb-M87789 1G GAMMA-1 CHAIN C PECTON (HUMAN);
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                                                                                                                                                                Vertebrata; Mammalia; Eutheria; Primates, Catarihini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image llnl gov) for further information Seq primer: 28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                Hiller, L. Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S. Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moorela, S., Schellenberg, K., Steptoe, M., Tan, F., Theising, R., White, Y., Wylie, T., Waterston, R., and Wilson, P., Theising, R., Washu-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 cactetacatggggetgageetgagettgagatetgaggacaeggeeetgtattaetgtgega 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 caaggtacgcacagaagttccagggcagagtcaceetgaeeagggacateeacgagea 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1...>266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares ovary tumor NbHOT"
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Pred. No. 1.09e-107;
0; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          rel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                   WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.6%;
Best Local Similarity 82,5%;
Matches 99; Conservative
                                                                                                                                                                                                    (bases 1 to 266)
                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                      Homo sapiens
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                                                                                                   human.
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                                        ACCESSION
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                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mPNA
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SOURCE
                                                                           KEYWORDS
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Adms, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gorgayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wei, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Huphes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, T.L., Govqhaqen, N.S.,
Glodek, A., Geldin, C.L., Hanna, M.C., Houkle, B. S.H.,
Kelley, J.M., Kolley, J.C., Luu, L.-I., Marmaros, S.M., Meritek, J.M.,
Morenc-Palanques, R.F., McDonald, L.A., Nquyen, D.L., Felliqrino, S.M.,
Phillips, C.A., Fyder, S.E., Scoff, T.E., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Qutterback, T.R., Weidman, J.F., Li, Y.,
Pednarik, D. P. God, L. Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Namali, K.V., Spriggs, T.A., Qutterback, T.R., Weidman, J.F., Li, Y.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P. Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H.,
Krymond, L., Weiz, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
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2V49b02.11 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756949
5° similar to qb·M87789 16 GAMMA-i CHAIN C REGION (HUMAN);.
A4428970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human General (http://www.tigr.org/tdb/hoi/hgi.html)
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Eukaryotae: mitochendrial eukaryotes; Metazoa: Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae:
Vertebrata; Mammalia; Butheria; Primates; Catarrhini: Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /hote="Orquo: Lhymus: Vector: pBluescript SK-; Site_1:
EcoR; Site_2: XhoI"
/clone_lib="Thymus II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94. aygaycayotuytusaytotyyyyotyayytyayyaaqootyqqqqootootnatqqtot. 153
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9712 Medical Center Drive, Pockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 198;
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Pred No 6 23e-66;
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<1..>198
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Bult, C. J. Lee, N. H., Kirkness, E. F., Weinstock, K. G. Gorayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R. A., Cline, T. F., Cotton, M. D., Earle-Hughes, J., Fine, L. F.
Filtzgerald, L.M., Filtzhugh, W.M., Printoman, J. G., Geoghaden, N. S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblow, F. Hinkle, P. S. Jr.,
Kelley, J. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Merrino-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S. M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K. V., Sprigas, T. A., Interbeck, T. P., Weidman, J. F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D. F., Ferrino, A., Fischer, C., Hastings, G.A.,
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      Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucabe, T., Lary M., Le. N., Lennon, G., Marra, M., Martin, T., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theistog, B., White, Y., Wylie, T., Waterston, R., and Wilson, P., Theistog, B., Washu-wack Est Project 1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae, mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata, Mammalia, Eutheria, Frimates; Catarihini; Hominidae;
                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.
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EST69374 Lymph node I Homo sapiens cDNA 5' end similar to
immunoglobulin heavy chain, VDJ regions (GB·X67906)
AA360195
                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 gegggggetggttegaeeeetggggeeagggaaeeetggteaeegteteetea 160
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                                                                                                                                                                          Contact: Wilson RK
WashU-Merck EST Project
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Best Local Similarity 92.5%;
1 (bases 1 to 230)
Hillier,L., Allen,M
Kucaba,T., Lacy,M.,
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AUTHORS
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/note="Organ: lymph node; Vector: pBluescript SK·; Site_l:
CooR: Site_2: Xhol"
/Clone_lib="Lymph node I"
/dev_stage="adult"
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Adams M.E. Kerlavage A.R. Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Leco, N. H., Rirkman, R.D., Weinstock, R.G., Googane, J.D.,
White, S. Sitzo, N. H., Rizhagh, W.B., Friethman, J.L., Geoghagen, N.S.,
Flizgorald, L.M., Flizhagh, W.M., Pritchman, J.L., Geoghagen, N.S.,
Flizgorald, A.M., Cochem, C.L., Hanna, W.C., Hedolom, E.Hinkley, P.S.,
Kelley, J.M., Relley, T., McConald, L.A., Nayson, D.T., Pelligrino, S.M.,
Phillips, C.A., Pyder, S.S., Soctt, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Sprigas, T.A., Utterback, T.R., Weidman, J.E., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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He.W W., Hh.J S., Greene, J.M., Gruber, J., Hudson, P., Kim, A. R.,
Kozak, D. I., Kunsch, C., Hungjun, J., Li H., Meissner, P. S., Olsen, H.,
Baymond, L., Wel, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M.,
Dillion, P. J., Fannon, M. F., Posen, C. A., Haseltine, W. A., Fields, C.,
Fraser, C. M. and Venter, J. C.
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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The Institute for Genomic Research
9712 Mcdical Center Drive, Pockville, MD 20859 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                              Other_ESIS: THC169164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 3018699423
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence. Nature 377 (6547 Suppl), 3-174 (1995)
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Bult, C.J., Lee, N. H., Kirkness, E.F., Weinstock, K. G., Gocayne, T. D.,
Bult, C.J., Lee, N. H., Kirkness, E.F., Weinstock, K. G., Gocayne, T. D.,
Clayton, R. A., Cilne, T. S., Cotton, M. D., Earle-Hughes, J., Finc, L. D.,
Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S.,
Godek, A., Gnehm, C. L., Hanne, M. C., Hedblow, E., Hinkle, P. S. Tr.,
Kelley, J. M., Kelley, J. C., Lin, T. Marmaros, S. M. Merrick, J. M.
Morero-Palanques, P. F., Morphald, L. Saudek, D. W., Shiriny, P.,
Phillips, C. A., Pyder, S. F., Scott, J. L., Saudek, D. W., Shiriny, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi html) Seq primer: MI3 Reverse.
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastinas,G.A..
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,T., Li,H., Maissner,P.S., Olsen,H.
Raymond,L., Weily,Y.F., Wing,J.T. Xu,C., Yu,G.L., Puben,S.M.
Dillion,P.J., Fennon,M.R., Posen,G.A., Hassitine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
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ECORI: Site_2: XhoI"
/clone_lib="Testis tumor"
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EST100002 Paperreas timer I Home septems clay 6 and similar to
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<1..>273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
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Contact: Kerlavage, AR
Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 3018699423
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LOCUS AA2CC299 243 bp mANA had to 21-APR-1997
DEFINITION FSF6410 Lymph mode, subtracted Home sapiens cDNA 6 end similar to similar to immunoglobulin damma heavy chain, V(III) region (GR-003894).
Small.K.V. Spriqas,I.A., Uttorback,T.R., Weidman,J.F., Li,Y., Dimke,D., Penq. D., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Penq. D.-F., Ferrico,A., Pischer,C., Hastings,G.A., He,W. W., Hu, IS. Grone,I.M., Stuber, I. Hidson P. Kim A.K., Kozak,D.L., Kunsch,C., Hundjun,J., Li,H., Meissner,P.S., Olsen,H., Baymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Ennon,M.K., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gone diversity and expression patterns based upon 83 million uncleotides of CDNA sequence.
Nature 377 (6547 Suppl), 3-174 (1995)
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/noto="Organ: pageras; Vortor: pkhueseript SK-; Site_i;
EcoRi; Site_2: Xhol"
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Admss.K.D., Forlavage, A.P., Fleischmann, R.D., Fuldmer, R.A.,
Pollt, C. 1 Herby, F. Filtmes, E.E., Weinstock, R.D., Guldyne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C.,
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Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidue;
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Pred. No. 1.01e:39;
0; Mismatches 71; Indels 9;
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The Institute for Genomic Research
7712 Medical Center Drive, Reckville, Mty 20850 USA
Tel: 3018699056
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Best Local Similarity 61.0%;
Matches 111; Conservative
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Clayton, P. A. Cline, T. F., Cotton, M. D., Earle-Hughes, T. Fince, D., Fitzerald, L. M., Fitzhugh, W. M., Fritchman, J. J., Geoghagen, N. S., Glodek, A., Gohm, C. L., Hanna, M. C., Hadhlome, Hinke, E. Hinkler, B. S., Kelley, J. G., Liu, L. I., Marmarcs, S. M., Merrick, J. M., Moreno-Palanques, P. F., McDonald, L. A., Nouyen, D. T., Pelligrino, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Sandak, D. M., Shilay, P., Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, F. Li, Y. Bednarik, D. P., Cac, L., Cageda, M. A., Fischer, C., Hastings, G. A., Dimke, D., Fengy, D. F., Perrie, A., Fischer, C., Hastings, G. A., Rawmond, L., Wu, S., Creene, M., Gruber, T., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P. S., Olsen, H., Paymond, L., Wan, Y. F., Wing, J., Xu, C., Yu, G. L., Popen, S. M., Pischer, J. C., Masser, C. M. and Venter, J. C., Nach, C., Masser, C. M. and Venter, J. C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence.
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AA326955
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/note="Organ: lymph node. Vector. pBluescript SK:: Site_1.
ECOPI: Site_2: XheT"
/clone_lib=Tlymph node, subtracted"
/love_stage="adult"
/love_stage="adult"
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, T.D.,
White, O., Sutton, G., Blake, J.A., Brandon B.C., Man-Wai C.,
Clayton, R.A., Cline, T.P., Cothron, D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhoph, W.M., Fritchman, T.L., Georhagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkie, P.S. Tr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone availability, additional sequence and expression information related to this ESI, please check the IIGR Human Gene Index (http://www.tigr.org/tdb/hqi/hqi.html)
Seq primer: M13 Reverse.
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Vertebrata; Mammalla; Butherla; Primates; Catarrhini; Hominidae,
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Best Local Similarity 66.7%; Pred. No. 1.29e-32;
Matches 78; Conservative 6, Mismatches 39, Indels 0, Gaps
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9712 Medical Center Drive, Pockville, MP 20850 USA
Tel: 3018699056
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AUTHORS

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Relloy, I M. Relloy, I.C. High, L. L. Marmaros, S.M., Morreno-Palanques, R.F. McDonald, L.A., Mguyen, D.T., Pelligrino, S.M., Phillips, C.A. Pyder, S.B. (Sandel), M. Ehirley, R., Small, K.V., Spriggs, T.A., Utterhack, T.P., Werdman, T.F., Li, Y., Dirke, D., Peng, D.-F. Ferries, A. Coleman, T.A., Collins, E.J., Pirke, D., Peng, D.-F. Ferries, A. Telscher, C., Hastings, G.A., Haw, W., Hu, T.S., Green, J.M., Gruber, I., Hudson, P.S., Olsen, H., Krask, D.L., Welly, T.F., Wing, J., Xu, C., Yu, G.L., Pupen, S.M., Pillion, P.J., Pannon, M. P. Posen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                    Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: MI3 Reverse.
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EcoRI. Site_2: XhoI"
/clone_lib="Colon I"
<love_stage="adult"
<love.stage="adult"
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Eukaryotae, mitochoudial eukaryotes, Metazoa, Chordata:
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Best Local Similarity 63.9%; Pred. No. 7.078-31;
Matches 85: Conservative 0: Mismatches 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_ESTs: THC167575
Contact: Kerlavage, AR
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Email: arkerlay
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Glodek, A. Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J. M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Marrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nquyen, T. Felligrino, S.M., Phillips, C.A., Ryder, S.E., Scolt, J.L., Saudek, D.M., Shirley, P. Ander, S.E., Scolt, J.L., Saudek, D.M., Chiley, P. Bednarik, D.P., Coleman, J.F., Li, Y. Bednarik, D.P., Copenan, T.M., Collins, E.J., Dimke, D.Fengo, D.F., Ferrico, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, T. Hudson, P. Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fander, G.M., Raseltine, W.A., Fields, C.
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Bult, C.J., Lee, N.H., Kirkness, F.F., Weinstock, R.G., Gorayno, T.D.,
White, O., Sutton, G., Rlake, J.A., Rrandon, P.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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Pred No 3.75e-29;
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9712 Medical Center Drive, Pockville. MD 20850 USA
Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: arkerlavētigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kerlavage, AR
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Best Local Similarity 64.3%;
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Relley I M., Kelley, I C., Liu L. J., Marmares, S.M., Merrek, J.M., Kelley, I K., Kelley, I C., Liu L. J., Marmares, S.M., Merrek, J.M., Mayere, Palanques, F.F., Mernald, L.A., Nauger, D.T., Pelliquino, S.M., Phillips, G. A., Kayer, F.F., Kelley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Woidman, I.F., Liu, Y., Prings, T.A., Utterback, T.R., Woidman, I.F., Liu, Y., Prings, D. Capeda, M.A., Coloman, T.A., Collins, P.J., Pinke, D., Kepada, M.A., Collins, P.J., Rozak, D.L., Kunsch, C., Hundjun, J., Li, H., Moissnor, P.S., Olsen, H., Paymond, L., Welly, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pillidon, P.J., Fannoo, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
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Fritchman, 1 , Geoghaden, N.S.,
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/dev_stage="adult, 20 yrs"
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Pred. No. 9.49e-26;
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     Fitzhugh, w.m.
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     Fitzaerald, L M
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Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim.A.K., Kozak,P. L., Kunsch,C. Hungjun, J. Li,H. Meissner,P.S., Olsen,H., Raymond,L., Weil,Y.F. Wing,J., Xu,C., Yu,G. L. Ruhen,S.M., Dillion,P.J. Fannen,M. F. Pischen, C. Ruhen,S.M., Fields,C., Fraser,C.M. and Venter,J.C. Pischen, G. W., Fields,C., Fraser,C.M. and Venter,J.C. A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C. and quen quene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi html) Seq primer: MI3 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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/note="Vector pRlueseript SK+, Site_1 EreRI; Site_2
XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 titgeactgicitetactggciceateagiaectainactggagtiggailegaeaginie 171 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
TTEL: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 others
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/cell_type="T-iymphocyte"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 9.0%;
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